GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2004, 19:58:03 ; Search time 22 Seconds
(without alignments)
729.498 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 1242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875	70.5	168	4	US-09-148-545-280	Sequence 280, App
2	800	64.4	155	4	US-09-621-976-3888	Sequence 3888, Ap
3	457	36.8	88	4	US-09-513-999C-4221	Sequence 4221, Ap
4	367	29.5	74	4	US-09-148-545-198	Sequence 198, App
5	86.5	7.0	5032	4	US-09-538-092-979	Sequence 979, App
6	86	6.9	17	4	US-09-148-545-279	Sequence 279, App
7	85.5	6.9	213	4	US-09-328-352-6122	Sequence 6122, Ap
8	83.5	6.7	440	4	US-09-489-039A-10833	Sequence 10833, A
9	83	6.7	472	4	US-09-252-991A-20457	Sequence 20457, A
10	83	6.7	635	4	US-09-252-991A-16721	Sequence 16721, A
11	81.5	6.6	522	4	US-09-461-325-220	Sequence 220, App
12	81.5	6.6	522	4	US-10-012-542-220	Sequence 220, App
13	81.5	6.6	522	4	US-10-115-123-220	Sequence 220, App
14	81.5	6.6	533	4	US-09-107-532A-6006	Sequence 6006, Ap
15	81.5	6.6	555	4	US-09-461-325-251	Sequence 251, App
16	81.5	6.6	555	4	US-10-012-542-251	Sequence 251, App
17	81.5	6.6	555	4	US-10-115-123-251	Sequence 251, App
18	79.5	6.4	590	3	US-08-743-168B-43	Sequence 43, Appl
19	79	6.4	608	3	US-09-413-814-92	Sequence 92, Appl
20	79	6.4	885	2	US-08-500-857A-8	Sequence 8, Appli
21	79	6.4	1213	3	US-09-413-814-79	Sequence 79, Appl
22	78	6.3	580	3	US-09-188-930-307	Sequence 307, App
23	78	6.3	580	4	US-09-312-283C-307	Sequence 307, App
24	78	6.3	705	3	US-09-134-001C-5356	Sequence 5356, Ap
25	77.5	6.2	269	3	US-09-134-001C-3461	Sequence 3461, Ap
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27	77.5	6.2	825	4	US-09-489-039A-11003	Sequence 11003, A
28	77	6.2	332	4	US-09-248-796A-20189	Sequence 20189, A
29	76.5	6.2	780	4	US-09-252-991A-32892	Sequence 32892, A
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33	76	6.1	568	5	PCT-US94-04496-30	Sequence 30, Appl
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37	76	6.1	712	2	US-09-060-692-64	Sequence 64, Appl
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45	75	6.0	324	3	US-09-134-001C-4774	Sequence 4774, Ap

ALIGNMENTS

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; Sequence 280, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05

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;  EARLIER APPLICATION NUMBER: 60/056,884
;  EARLIER FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 280
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
;   LENGTH: 168

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RESULT 2
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; Sequence 3888, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
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;   NAME/KEY: SIGNAL
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RESULT 3
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; Sequence 4221, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
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RESULT 4
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; Sequence 198, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 70 Human Secreted Proteins
;  FILE REFERENCE: PZ001P1
;  CURRENT APPLICATION NUMBER: US/09/148,545
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/US98/04482
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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;  EARLIER APPLICATION NUMBER: 60/056,887
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;  EARLIER APPLICATION NUMBER: 60/057,650
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/056,884
;  EARLIER FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 280
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
;   LENGTH: 74

  Query Match             29.5%;  Score 367;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-34;
  Matches   74;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        169 MVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSS 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSS 60

Qy        229 GSSKTGKSGAGKRR 242
              ||||||||||||||
Db         61 GSSKTGKSGAGKRR 74


RESULT 5
US-09-538-092-979
; Sequence 979, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 979
;   LENGTH: 5032
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P21817
US-09-538-092-979

  Query Match              7.0%;  Score 86.5;  DB 4;  Length 5032;
  Best Local Similarity   22.3%;  Pred. No. 27;
  Matches   68;  Conservative   29;  Mismatches   95;  Indels  113;  Gaps   14;

Qy          5 LWGFF----------PVLLLLLLSG--DVQSSEVPG------------AAAEGSGGSGV 39
              |||              | :  ||:|   |  | ||| |              |:||:| :
Db       4352 LWGSLFGGGLVEGAKKVTVTELLAGMPDPTSDEVHGEQPAGPGGDADGEGASEGAGDAAE 4411

Qy         40 GIGDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDI---------- 89
              | ||  :    |  |          |  : ||    |  : :|:  :  |:
Db       4412 GAGDEEEAVHEAGPGGA------DGAVAVTDG----GPFRPEGAGGLGDMGDTTPAEPPT 4461

Qy         90 PSGSYVVE----------------VVSPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVR 133
              | || :::                |  :| : |  :  |            | |
Db       4462 PEGSPILKRKLGVDGVEEELPPEPEPEPEPELEPEKADAENGEK------------EEVP 4509

Qy        134 LPYPLQMKSSGPPSYFIKRES-----WG--------WTDFLMNPMVMMMVLPLLI----- 175
              |  |   |   |||   |:|      ||        : ::|      :  | | :
Db       4510 EPTPEPPKKQAPPSPPPKKEEAGGEFWGELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN 4569

Qy        176 FVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGK 235
              |:||   |: | |    :|| |                       :   ||  | ||| |
Db       4570 FILLFYKVSDSPPG-EDDMEGSA-------------------AGDVSGAGSGGSSGWG- 4607

Qy        236 SGAGK 240
              |||:
Db       4608 LGAGE 4612


RESULT 6
US-09-148-545-279
; Sequence 279, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 70 Human Secreted Proteins
;  FILE REFERENCE: PZ001P1
;  CURRENT APPLICATION NUMBER: US/09/148,545
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/US98/04482
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
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;  EARLIER APPLICATION NUMBER: 60/040,333
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;  EARLIER APPLICATION NUMBER: 60/047,613
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 279
; LENGTH: 17

Query Match 6.9%; Score 86; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        105 FDPVRVDITSKGKMRAR 121
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Db          1 FDPVRVDITSKGKMRAR 17
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RESULT 7
US-09-328-352-6122
; Sequence 6122, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6122
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6122

Query Match 6.9%; Score 85.5; DB 4; Length 213;
Best Local Similarity 21.5%; Pred. No. 0.25;
Matches 42; Conservative 37; Mismatches 47; Indels 69; Gaps 11;

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Qy         42 GDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGS-----FVVHDIPSGSYVV 96
              | : : :|| |       :|          |: ||:: | :     |:        ::
Db          2 GIKMRDQGRLV-------EWFD--------EKGYGFIQPDDAEKERVFL--------HIK 38

Qy         97 EVVSPAYRFDPV-------RVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKSS------ 143
              :   | |  |:        | :  :|: ||: | |:| |:  :   | : :||
Db         39 DFARPGPR--PIIGCALEYLVILDERGRFRAQQVTYLKASQTRKASKPAKTQSSFQASPW 96

Qy        144 -----GPPSYFIKRESWGWTDFLMNPMVMMMVLP--LLIFVLLPKVVN----TSDPDM-- 190
                  |   ||:           ||  |  : :||   |:|||:  |::    : | :
Db         97 SAMQMGIVFYFV----------LMGIMSFIHILPAYTLLFVLMMNVLSYWLYSQDKEAAQ 146

Qy        191 ---RREMEQSMNMLN 202
                ||  ||::::::
Db        147 LGNRRVPEQTLHIVS 161

RESULT 8
US-09-489-039A-10833
; Sequence 10833, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10833
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10833

Query Match 6.7%; Score 83.5; DB 4; Length 440;
Best Local Similarity 24.6%; Pred. No. 1.3;
Matches 44; Conservative 18; Mismatches 56; Indels 61; Gaps 5;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              || :| | ||      ||| |  :||  | | |      |:|  :     ||       |
Db        284 MAKSLAGGFP------LSGVVGRAEVMDAPAPG------GLGGTYAGNPLAVAAAHAVLD 331

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
                |:  ::    |:                  ||:: ||:: |    |  ||:  :| | |
Db        332 VIAEEQLCQRAEQ----------------LGSHLQEVLNQARATCPAIVDVRGRGSMVA 374

Qy        121 RYVNYIKTSE-------------------------VVRLPYPLQMKSSGPPSYFIK 151
                |  :| |                        |:|  ||| :    | : | |
Db        375 VEFNDPQTGEPSPEFTRQVQQKAQENGLLLLSCGVYGNVIRFLYPLTI----PDAQFSK 429
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RESULT 9
US-09-252-991A-20457
; Sequence 20457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20457
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20457

Query Match 6.7%; Score 83; DB 4; Length 472;
Best Local Similarity 21.5%; Pred. No. 1.7;
Matches 53; Conservative 33; Mismatches 91; Indels 70; Gaps 10;

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Qy          8 FFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAARV 67
              | |||  :     : :   |||| :  ||  :       ::|         |   |  |
Db        198 FHPVLRTVAFR--LLARTPPGAARQSQGGPMI------RLE--------KVNKWYGAYHA 241

Qy         68 LVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVR--------VDITSKGKMR 119
              | | :| ||      |  ||   ||||    ::    | :|::          || : |
Db        242 LADVDEQVG----RGEVVVVCGPSGSGKSTLIRTLNRLEPIQGGRILIDGQDIHAPGLDL 297

Qy        120 ARYVNYI--KTSEVVRLPY----------PLQMKSSGP------------------PSY 148
                |: ::|     :    |:          ||:::   |                    :
Db        298 NRFRSHIGFVFQQFNLFPHLNVLDNCTLAPLRLRGLKPAEARRQALALLERVGLADKAAA 357

Qy        149 FIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREM--------EQSMNM 200
              | | | |     :   : |  ||::|    :  :  ||:|  |:           | |
Db        358 FPARLSGGQQQRVAIARALAMEPPLMLF---DEPTSALDPEMVGEVLLVMRDLARDGMTM 414

Qy        201 LNSNHEL 207
                :  ||:
Db        415 VVVTHEM 421

RESULT 10
US-09-252-991A-16721
; Sequence 16721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16721
; LENGTH: 635
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```

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;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16721

  Query Match             6.7%;  Score 83;  DB 4;  Length 635;
  Best Local Similarity   32.7%;  Pred. No. 2.7;
  Matches   34;  Conservative   10;  Mismatches   42;  Indels   18;  Gaps    6;

Qy         24 SEVPGAAAEG--SGGSGVGIGDRFKIEGRA--VVPGV----KPQDWISAARVLVDGEEHV 75
              : | |||  |  | | | |:     :|| |   | ||      :  |   | :  |||||
Db        196 AHVRGAAEAGQASAGDGGGMAVAVDLEGSADEQVDGVLSCQLAEHPIGTQRAVATGEEHV 255

Qy         76 GFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMR 119
              | |   |   :|         | |   :  ||  :|   ||::|
Db        256 GTL---GDVALH----AQLGAEAV---HALDPAALDGGDKGRVR 289


RESULT 11
US-09-461-325-220
; Sequence 220, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
;  EARLIER APPLICATION NUMBER: 60/090,113
;  EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-461-325-220

  Query Match             6.6%;  Score 81.5;  DB 4;  Length 522;
  Best Local Similarity   25.2%;  Pred. No. 2.9;
  Matches   29;  Conservative   22;  Mismatches   51;  Indels   13;  Gaps    4;

Qy        112 ITSKGK-MRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIK------RESWGWTDFLMNP 164
              ||||||  :  |::|    : :: |: |:|    | :   |       |    ||::  :|
Db        346 ITSKGKENKPSYIHYQPAQDRLQ-PHLLEMLIQLPANSVTKVSIQFERALLKWTEYTPDP 404

Qy        165 MVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFS 219
                | | ::  |:| :|      |       :   : ||   : | | :  ||::
Db        405 NHGFYVSPSVLSALVPSMVAAKPVDW-----EESPLFNSLFPVSDGSNYFVRLYT 454


RESULT 12
US-10-012-542-220
; Sequence 220, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-012-542-220

  Query Match             6.6%;  Score 81.5;  DB 4;  Length 522;
  Best Local Similarity   25.2%;  Pred. No. 2.9;
  Matches   29;  Conservative   22;  Mismatches   51;  Indels   13;  Gaps    4;

Qy        112 ITSKGK-MRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIK------RESWGWTDFLMNP 164
              ||||||  :  |::|    : :: |: |:|    | :   |       |    ||::  :|
Db        346 ITSKGKENKPSYIHYQPAQDRLQ-PHLLEMLIQLPANSVTKVSIQFERALLKWTEYTPDP 404

Qy        165 MVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFS 219
                | | ::  |:| :|      |       :   : ||   : | | :  ||::
Db        405 NHGFYVSPSVLSALVPSMVAAKPVDW-----EESPLFNSLFPVSDGSNYFVRLYT 454


RESULT 13
US-10-115-123-220
; Sequence 220, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-115-123-220

  Query Match             6.6%;  Score 81.5;  DB 4;  Length 522;
  Best Local Similarity   25.2%;  Pred. No. 2.9;
  Matches   29;  Conservative   22;  Mismatches   51;  Indels   13;  Gaps    4;

Qy        112 ITSKGK-MRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIK------RESWGWTDFLMNP 164
              ||||||  :  |::|    : :: |: |:|    | :   |       |    ||::  :|
Db        346 ITSKGKENKPSYIHYQPAQDRLQ-PHLLEMLIQLPANSVTKVSIQFERALLKWTEYTPDP 404
```

```
Qy        165 MVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFS 219
              | | ::  |:| :|     |      :   : ||   : | | :  ||::
Db        405 NHGFYVSPSVLSALVPSMVAAKPVDW-----EESPLFNSLFPVSDGSNYFVRLYT 454


RESULT 14
US-09-107-532A-6006
; Sequence 6006, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 6006:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 533 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...533
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6006:
US-09-107-532A-6006

  Query Match             6.6%;  Score 81.5;  DB 4;  Length 533;
  Best Local Similarity   17.3%;  Pred. No. 3;
  Matches   29;  Conservative   20;  Mismatches   36;  Indels   83;  Gaps    4;

Qy         30 AAEGSGGGSGVG---------IGDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKT 80
              ||    | | |         ||| : || || | |:     |                 |
Db        144 AARAIQGMGAGAMMPVALTIIGDLYSIEKRAKVLGLNSSAW-------------GIASV 189

Qy         81 DGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQM 140
               |        :| ::|| :
Db        190 FGPL------AGGFIVETI---------------------------------------- 202

Qy        141 KSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDP 188
                          || |  |:  |: ::::: : :::  ||::: | |
Db        203 ------------SWHWIFFINVPIGILLIILIWLYLNEPKIIHESKP 237


RESULT 15
US-09-461-325-251
; Sequence 251, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
;  EARLIER APPLICATION NUMBER: 60/090,113
;  EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 251
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (555)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-461-325-251

  Query Match             6.6%;  Score 81.5;  DB 4;  Length 555;
  Best Local Similarity   25.2%;  Pred. No. 3.2;
  Matches   29;  Conservative   22;  Mismatches   51;  Indels   13;  Gaps    4;

Qy        112 ITSKGK-MRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIK------RESWGWTDFLMNP 164
              ||||||  :  |::|    : :: |: |:|    | :   |       |    ||::  :|
Db        345 ITSKGKENKPSYIHYQPAQDRLQ-PHLLEMLIQLPANSVTKVSIQFERALLKWTEYTPDP 403

Qy        165 MVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFS 219
                  | | ::  |:| :|     |       :   : ||   : | | :  ||::
Db        404 NHGFYVSPSVLSALVPSMVAAKPVDW-----EESPLFNSLFPVSDGSNYFVRLYT 453


Search completed: December 24, 2004, 20:21:39
Job time : 23 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2004, 19:59:48 ; Search time 68 Seconds
(without alignments)
342.418 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 1242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	390.5	31.4	344	2	S72578	hypothetical prote
2	194.5	15.7	198	2	H84646	hypothetical prote
3	102.5	8.3	189	2	T40699	hypothetical prote
4	94	7.6	259	2	B95267	probable ABC trans
5	93.5	7.5	526	2	T13687	hypothetical prote
6	91.5	7.4	896	2	S76064	hypothetical prote
7	87.5	7.0	889	2	E87304	TonB-dependent rec
8	86.5	7.0	5032	1	A35041	ryanodine receptor
9	85.5	6.9	1482	2	S13495	pregnancy zone pro
10	84.5	6.8	712	2	B47021	pectic enzyme secr
11	83.5	6.7	763	2	T24367	hypothetical prote
12	83.5	6.7	896	2	S59990	phycobilisome anch
13	83	6.7	441	2	B49837	clathrin-associate
14	83	6.7	459	2	C85017	probable CAAX pren
15	83	6.7	695	2	AE1406	translation elonga
16	83	6.7	695	2	AE1782	translation elonga
17	82.5	6.6	692	2	B69628	translation elonga
18	82	6.6	693	2	E89822	translational elon
19	81.5	6.6	145	2	T04632	hypothetical prote
20	81.5	6.6	428	2	G86240	hypothetical prote
21	81.5	6.6	442	2	T18917	hypothetical prote
22	81.5	6.6	1190	2	S21977	Pm5 protein - huma
23	81.5	6.6	1446	2	T30916	carboxypeptidase D
24	80	6.4	493	2	T33569	hypothetical prote
25	79.5	6.4	316	2	T01712	hypothetical prote
26	79.5	6.4	369	2	B87645	HlyD family secret
27	79.5	6.4	380	1	VCVGCN	coat protein - cuc
28	79.5	6.4	721	2	T41530	hypothetical prote
29	79.5	6.4	734	2	T42588	DNA-packaging prot
30	79.5	6.4	1244	2	T49632	hypothetical prote
31	79	6.4	331	2	C90486	ABC transporter, A
32	79	6.4	485	2	D70142	glu-tRNA amidotran
33	79	6.4	557	2	T49900	2-oxoglutarate/mal
34	79	6.4	885	2	S36601	pyruvate, phosphat
35	78.5	6.3	419	2	AC1049	HflK protein [impo
36	78.5	6.3	436	2	E70387	conserved hypothet
37	78.5	6.3	472	2	B99372	multidrug resistan
38	78.5	6.3	559	2	C84137	transcription regu
39	78	6.3	317	2	H89893	hypothetical prote
40	78	6.3	400	2	F75275	chromate transport
41	77.5	6.2	177	2	A99469	conserved hypothet
42	77.5	6.2	380	2	AH2232	hypothetical prote
43	77.5	6.2	425	2	JE0086	SH3-domain binding
44	77.5	6.2	550	2	F90407	molybdopterin bios
45	77.5	6.2	777	2	C86454	hypothetical prote

ALIGNMENTS

RESULT 1
S72578
hypothetical protein C35D10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 31-Oct-1997
C;Accession: S72578
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, J
ulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johnston, L.; Jone
, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.
submitted to the EMBL Data Library, February 1995
A;Authors: Shownkeen, R.; Smaldon, N.; Smith, A.; Sonnhammer, E.; Staden, R.; Sulston, J.
proat, J.; Wohldman, P.
A;Description: The C. elegans genome project: Contiguous nucleotide sequence of over two
A;Reference number: S72566
A;Accession: S72578
A;Molecule type: DNA
A;Residues: 1-344 <WIL>
A;Cross-references: EMBL:U21324; NID:g687879; PID:g687880
A;Experimental source: strain Bristol N2
C;Genetics:
A;Map position: 3
A;Introns: 37/3; 111/1; 144/3; 158/1; 235/3; 289/2
A;Note: C35D10.1

Query Match 31.4%; Score 390.5; DB 2; Length 344;
Best Local Similarity 40.9%; Pred. No. 3.6e-27;
Matches 74; Conservative 48; Mismatches 52; Indels 7; Gaps 3;

```
Qy         62 ISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRAR 121
              : :||: ::  :::||:: | :| |  :|:|:|:|:: :  : |:|:||||||||||||||
Db        170 VRSARIHLNHGQYMGFVRQDCTFRVDFVPTGTYIVQIENTDFVFEPIRVDITSKGKMRAR 229

Qy        122 YVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPK 181
              :  :: : |  ||||||:: : ||  || ||| |  || | :|||:|:|:||:: ::|||
Db        230 KLTILQPNNVNTLPYPLRLSARGPARYFRKREEWRITDMLFSPMVLMLVVPLVVMLILPK 289

Qy        182 VVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKR 241
              :  :||::::|||   ||     ::||| | |   |  :  |     : || ||:|:|
Db        290 -MTANDPELKKEME---NMQMPKVDMPDVGEMMANFFGGSAPAKK---KAVTGGSGSGQR 342

Qy        242 R 242
              |
Db        343 R 343
```

RESULT 2
H84646
hypothetical protein At2g25310 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84646
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84646
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <STO>
A;Cross-references: UNIPROT:Q9SIR2; GB:AE002093; NID:g4567246; PIDN:AAD23660.1; GSPDB:GN
C;Genetics:
A;Gene: At2g25310
A;Map position: 2
C;Superfamily: Arabidopsis hypothetical protein F10N7.60

Query Match 15.7%; Score 194.5; DB 2; Length 198;
Best Local Similarity 25.6%; Pred. No. 5.9e-10;
Matches 43; Conservative 46; Mismatches 48; Indels 31; Gaps 5;

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Qy         40 GIGDRFKIEGRAVVPGVKPQDWI------SAARVLVDGEEHVGFLKTDGSFVVHDIPSGS 93
Db         34 GSEDSYTITGRVKIP---PSNVIGHIAKFSNVKVILNGGQKITFLRPDGYFTFHEVPAGT 90

Qy         94 YVVEVVSPAYRFDPVRVDITS--KGKMRARYVNYIKT-SEVVRLPYPLQMKSSGPPSYFI 150
Db         91 HLIEVSAMGYFFSPVRVDVSARHRGKVQATLTETRRSLTELIREPFNIM---------- 139

Qy        151 KRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSM 198
Db        140 --------SIVKSPMGLMVGFMVVVVFLMPKLMENIDPEEMKQAQEEM 179
```

RESULT 3
T40699
hypothetical protein SPBC83.10 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40699
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21945
A;Accession: T40699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-189 <WOO>
A;Cross-references: UNIPROT:O94694; EMBL:AL035536; PIDN:CAB36872.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; cosmid c83
C;Genetics:
A;Gene: SPDB:SPBC83.10
A;Map position: 2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC83.10

Query Match 8.3%; Score 102.5; DB 2; Length 189;
Best Local Similarity 19.4%; Pred. No. 0.094;
Matches 36; Conservative 39; Mismatches 76; Indels 35; Gaps 4;

```
Qy          9 FPVLLLLLLSGDVQSS---EVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAA 65
Db          6 FLLLSVLCFAGCIQQSLQAEVYG----------------KVLTNTILPKINLLSYDTRA 48

Qy         66 RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDI---------TSKG 116
Db         49 RLISSNKTFETVVERDGSFTFPNVPDEIYFLRLESIDYEFSEFHIIINESIVYPYYTSPA 108

Qy        117 KMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIF 176
Db        109 EKRP------ASSTAKNTSYPIKVRAVLKRDYLKEPRKFSLIRLLKSPMMLLSLASVVLV 162

Qy        177 VLLPKV 182
Db        163 FILPKL 168
```

RESULT 4
B95267
probable ABC transporter ATP-binding protein SMa0083 [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95267
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <KUR>
A;Cross-references: UNIPROT:Q931A2; GB:AE006469; PIDN:AAK64700.1; PID:g14523100; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMa0083
A;Genome: plasmid
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 7.6%; Score 94; DB 2; Length 259;
Best Local Similarity 21.3%; Pred. No. 0.81;
Matches 44; Conservative 30; Mismatches 61; Indels 72; Gaps 9;

```
Qy         39 VGIGDRFKIEG------RAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSG 92
Db         43 VGRGERIVICGPSGSGKSTLIRCINQLETIHSGRIVVDG--------------HDLTAG 87

Qy         93 SYVVEVVSPA-----YRFD--------------PVRVDITSKGKMRARYVNYIKTSEVVR 133
Db         88 GRNVDLVRQETGMVFQQFNLFPHMTVLENCTLAPMKVRGLAKAEAEETAMKYLKR---VR 144

Qy        134 LP-----YPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDP 188
Db        145 IPEQAVKYPAQLSGGQQQRVAIARA------LCMNPKIMLFDEP----------TSALDP 188

Qy        189 DMRREM--------EQSMNMLNSNHEL 207
Db        189 EMVKEVLDTMVDLANEGMTMLCVTHEM 215
```

RESULT 5
T13687
hypothetical protein EG0003.1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13687
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17699
A;Accession: T13687
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-526 <MUR>
A;Cross-references: UNIPROT:O96825; EMBL:AL031863; NID:e1331652; PID:e1331662; PIDN:CAA21
C;Genetics:
A;Cross-references: FlyBase:FBgn0025833
A;Introns: 314/2; 455/1; 485/3
A;Note: EG:EG0003.1

Query Match 7.5%; Score 93.5; DB 2; Length 526;

Best Local Similarity 24.2%; Pred. No. 2.2;
Matches 54; Conservative 30; Mismatches 90; Indels 49; Gaps 9;

```
Qy         23 SSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDG 82
              |: : |::: |||| ||| |:          | |  ::     |  ||     |
Db        237 STPISGSSSSSGSGGGGVGNGN----------GSVPSGMMTPTHT-YPGRRHVKNRLMD- 283

Qy         83 SFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKS 142
                : : :|    : |  |||    |  | :::    | ||  | |:|     |   :  |
Db        284 --IQNRLPP---IKEFRSPAKVPHPSPVHVSNP---RFRYSTYTKSSAHELAPLLRESGS 335

Qy        143 SGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLN 202
              | ||    :| |          || : :    |             |   :     :  |
Db        336 SPPP----RRPS---------PMNIQLSCSALA-----------PPPLKAGGAKICPLT 370

Qy        203 SNHELPDVSEFMTRLFSSKSS---GKSSSGSSKTGKSGAGKRR 242
              | : ||  :  | :     :|   ||::  :||:   |||  |
Db        371 SKNSLPKNAYVMPKDKKQPASVPQGKATGTASKSTPQGAGCSR 413
```

RESULT 6
S76064
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76064
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76064
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-896 <KAN>
A;Cross-references: UNIPROT:Q55544; EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA1004
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 7.4%; Score 91.5; DB 2; Length 896;
Best Local Similarity 22.4%; Pred. No. 6.6;
Matches 57; Conservative 34; Mismatches 85; Indels 79; Gaps 12;

```
Qy         18 SGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAAR---------- 66
              | | ::  |  | : ||||   |:   |   |  : || :|   |: ||
Db         99 SSDSRNGSVTYAESNGSGGLFGGLRSVFSSTG-PIPPGFRP---INIARYGPSNMQKSLR 154

Qy         67 ----------VLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSK 115
                       :| |: ::  : | |           : ||:  |  |  | |
Db        155 DMSWFLRYTTYAIVAGDPNIIVVNTRG----------LKEVIENACSIDATIVAIQ-- 200

Qy        116 GKMRARYVNYIKTS----EVV----------RLPYPLQMKSSG----------PPSYF- 149
              :|||   :| : :    |:|          : | |       |          | |||
Db        201 -EMRAASADYFRNNAQAKEIVLQYFDILLSEFKAPTPANKVRQGPSNDIQGLELPQSYFN 259

Qy        150 --IKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHEL 207
                 ||:      : | | :  :    :|     ::    : |: :   ||:: | |
Db        260 AAAKRQK-----YAMKPGLSALEKNAVIKAAYRQIF---ERDITKAYSQSISYLESQVRN 311

Qy        208 PDVS--EFMTRLFSS 220
               |:|  ||: ||  |
Db        312 GDISMKEFVRRLAKS 326
```

RESULT 7
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <STO>
A;Cross-references: UNIPROT:Q9AAZ6; GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN
C;Genetics:
A;Gene: CC0446

Query Match 7.0%; Score 87.5; DB 2; Length 889;
Best Local Similarity 22.9%; Pred. No. 15;
Matches 32; Conservative 23; Mismatches 54; Indels 31; Gaps 6;

```
Qy         24 SEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGS 83
              | ||     :|  | |  : :||:|:| |:|   |:    |::|               :
Db        508 STVPSNYLKGFDGVGTQMQNRFRIDGNAMVSYVESGKWLAAGAT----------MPKPSI 557

Qy         84 FVVHDIPSGSY-VVEVVSPAYRFDPVRVDITSKGKMRARY-VNYIKTSEVVRLPYPLQMK 141
              |   :  :|:: : | :     |      : |      :|  : | |:|||         :
Db        558 FAAAEFTAGNWNIQEDIDALYAQANFKAD-----NVRGNFGVRYVKTS----------VD 602

Qy        142 SSG----PPSYFIKRESWGW 157
              |:|    | :   |   | |
Db        603 SAGYVCKPGAACNKAADWSW 622
```

RESULT 8
A35041
ryanodine receptor type 1, skeletal muscle - human
N;Alternate names: calcium release channel protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35041; I84622; S66630
R;Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meissner, G.; M
J. Biol. Chem. 265, 2244-2256, 1990
A;Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) release
A;Reference number: A35041; MUID:90130482; PMID:2298749
A;Accession: A35041
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-5032 <ZOR>
A;Cross-references: UNIPROT:P21817; GB:J05200; NID:g337721; PIDN:AAA60294.1; PID:g337722
R;Otsu, K.; Phillips, M.S.; Khanna, V.K.; de Leon, S.; MacLennan, D.H.
Genomics 13, 835-837, 1992
A;Title: Refinement of diagnostic assays for a probable causal mutation for porcine and h
A;Reference number: I46644; MUID:92347887; PMID:1639409
A;Accession: I84622
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 598-722 <RES>
A;Cross-references: GB:M91455; NID:g337723; PIDN:AAA60295.1; PID:g553643
R;Lynn, S.; Morgan, J.M.; Lamb, H.K.; Meissner, G.; Gillespie, J.I.
FEBS Lett. 372, 6-12, 1995
A;Title: Isolation and partial cloning of ryanodine-sensitive Ca(2+) release channel prot
A;Reference number: S66630; MUID:96032536; PMID:7556644
A;Accession: S66630
A;Molecule type: mRNA
A;Residues: 4690-4968 <LYN>
A;Experimental source: myometrial smooth muscle
C;Genetics:
A;Gene: GDB:RYR1
A;Cross-references: GDB:120359; OMIM:180901
A;Map position: 19q13.1-19q13.1
A;Introns: 642/2
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog
C;Keywords: calcium channel; homotetramer; phosphoprotein; skeletal muscle; transmembrane
F;1788-1984/Domain: transcription initiation factor sigma region 1 homology <SR1>

Query Match 7.0%; Score 86.5; DB 1; Length 5032;
Best Local Similarity 22.3%; Pred. No. 1.7e+02;

```
  Matches   68;  Conservative   29;  Mismatches   95;  Indels  113;  Gaps   14;

Qy          5 LWGFF----------PVLLLLLLSG--DVQSSEVPG------------AAAEGSGGSGV 39
              |||              | :  ||:|  |  | || |             |:||:| :
Db       4352 LWGSLFGGGLVEGAKKVTVTELLAGMPDPTSDEVHGEQPAGPGGDADGEGASEGAGDAAE 4411

Qy         40 GIGDRFKIEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDI---------- 89
              | ||  :   |   |        |  : ||    |  : :|:  : |:
Db       4412 GAGDEEEAVHEAGPGGA------DGAVAVTDG----GPFRPEGAGGLGDMGDTTPAEPPT 4461

Qy         90 PSGSYVVE---------------VVSPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVR 133
              | || :::               |    :| : |  :  |            | |
Db       4462 PEGSPILKRKLGVDGVEEELPPEPEPEPEPELEPEKADAENGEK-----------EEVP 4509

Qy        134 LPYPLQMKSSGPPSYFIKRES-----WG--------WTDFLMNPMVMMMVLPLLI----- 175
              | |   |   |||   |:|      ||        : ::|      :  | | :
Db       4510 EPTPEPPKKQAPPSPPPKKEEAGGEFWGELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN 4569

Qy        176 FVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGK 235
              |:||   |: | |    :|| |                :   ||  | |||  |
Db       4570 FILLFYKVSDSPPG-EDDMEGSA-------------------AGDVSGAGSGGSSGWG- 4607

Qy        236 SGAGK 240
               |||:
Db       4608 LGAGE 4612


RESULT 9
S13495
pregnancy zone protein - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: S13495; S09106; A34230; PS0077; S21637
R;Devriendt, K.; van den Berghe, H.; Cassiman, J.J.; Marynen, P.
Biochim. Biophys. Acta 1088, 95-103, 1991
A;Title: Primary structure of pregnancy zone protein. Molecular cloning of a full-length
A;Reference number: S13495; MUID:91113734; PMID:1989698
A;Accession: S13495
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1482 <DEV>
A;Cross-references: UNIPROT:P20742; EMBL:X54380; NID:g35824; PIDN:CAA38255.1; PID:g35825
R;Marynen, P.; Devriendt, K.; van den Berghe, H.; Cassiman, J.J.
FEBS Lett. 262, 349-352, 1990
A;Title: A genetic polymorphism in a functional domain of human pregnancy zone protein:
n.
A;Reference number: S09106; MUID:90242963; PMID:1692292
A;Accession: S09106
A;Molecule type: DNA
A;Residues: 668-690,'M',692-753 <MAR>
A;Cross-references: EMBL:X51541
R;Sottrup-Jensen, L.; Sand, O.; Kristensen, L.; Fey, G.H.
J. Biol. Chem. 264, 15781-15789, 1989
A;Title: The alpha-macroglobulin bait region. Sequence diversity and localization of cle
A;Reference number: A34230; MUID:89380162; PMID:2476433
A;Accession: A34230
A;Molecule type: protein
A;Residues: 670-752,'Q',754-759 <SOT>
C;Genetics:
A;Gene: GDB:PZP
A;Cross-references: GDB:120330; OMIM:176420
A;Map position: 12p13-12p12.2
A;Introns: 73/3; 116/2; 146/3; 169/3; 703/1; 753/2
A;Note: the list of introns may be incomplete
C;Superfamily: alpha-2-macroglobulin
F;685-735/Region: bait region

  Query Match             6.9%;  Score 85.5;  DB 2;  Length 1482;
  Best Local Similarity   20.5%;  Pred. No. 44;
  Matches   54;  Conservative   43;  Mismatches   89;  Indels   77;  Gaps   14;

Qy         28 GAAAEGSGGSGVGIGDRFKI-------------EGRAVVP----GVKPQDWI-SAARVL 68
               ||  :|  |:|:|: :|  :             :    ||       |: ||     |

Db        694 GAVGQGYYGAGLGVVERPYVPQLGTYNVIPLNNEQSSGPVPETVRSYFPETWIWELVAVN 753

Qy         69 VDGEEHVGFLKTD-------GSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITS-----KG 116
                 |   ||     |       |:| : :       :   :    | |  |::|     :|
Db        754 SSGVAEVGVTVPDTITEWKAGAFCLSE--DAGLGISSTASLRAFQPFFVELTMPYSVIRG 811

Qy        117 K---MRARYVNYIKTSEVVRLPYPLQMKSS----------GPPSYFI---KRESWGWTDF 160
              :   ::|  :||:  : :|:   :|:|:|          |  || |   :|:: ||
Db        812 EVFTLKATVLNYL--PKCIRV--SVQLKASPAFLASQNTKGEESYCICGSERQTLSWT-- 865

Qy        161 LMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNML-NSNHELPDVSE----FMT 215
                                  : || :   :  :  |  ||: :  |   |:|::      |
Db        866 -----------------VTPKTLGNVNFSVSAEAMQSLELCGNEVVEVPEIKRKDTVIKT 908

Qy        216 RLFSSKSSGKSSSGSSKTGKSGA 238
              |  ::   :  : || |  |||
Db        909 LLVEAEGIEQEKTFSSMTCASGA 931


RESULT 10
B47021
pectic enzyme secretion protein OutD - Erwinia chrysanthemi
C;Species: Erwinia chrysanthemi
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: B47021
R;Lindeberg, M.; Collmer, A.
J. Bacteriol. 174, 7385-7397, 1992
A;Title: Analysis of eight out genes in a cluster required for pectic enzyme secretion by
A;Reference number: A47021; MUID:93054355; PMID:1429461
A;Accession: B47021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-712 <LIN>
A;Note: sequence extracted from NCBI backbone (NCBIP:118271)

  Query Match             6.8%;  Score 84.5;  DB 2;  Length 712;
  Best Local Similarity   22.1%;  Pred. No. 21;
  Matches   65;  Conservative   34;  Mismatches   98;  Indels   97;  Gaps   13;

Qy          5 LWGFFPV-----LLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVP--GVK 57
              ::||  |      :| :: | | :|| :| |  |        |:||         |||   |
Db         87 VYGFSVVPMDNGVLKVIRSKDAKSSSIPLANNEQP-----GVGDELVTR---VVPLNNVA 138

Qy         58 PQDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSG----------SYVVEVVSPAYRFD 106
               :|     | | |              |||  ||             :|::|:
Db        139 ARDLAPLLRQLND--------NAGAGTVVHYEPSNVLLMTGRAAVIKRLVDIVN------ 184

Qy        107 PVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQM---KSSGPPSYFIKRESWGWTDFLM- 162
              || |   :|    :||    :| :|    |      |:: | :      : | |: ::
Db        185 --TVDKTGDREMITVSLNYASAEDVAKLVNDLNKTDEKNALPSTMLANVVADGRTNSVVV 242

Qy        163 ------NPMVMMMVLPL----------LIFVLLPKVV--------------------NT 185
                   :|  : |:  |           :|::  | :                     |:
Db        243 SGEENTSPCAVEMIRQLDRKQVAQGGTKVIYLKYAKALDLIEVLAGNGTSGNRNSSSTNS 302

Qy        186 SDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAG 239
              | |   |    |  : |||             |  |||  || || :   | |
Db        303 SRPSSTR---SSSTLNNSNSS----------SSGSSSGSGSSSSSSSSSMGFG 342


RESULT 11
T24367
hypothetical protein T02E9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24367
R;Kershaw, J.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19882
A;Accession: T24367
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-763 <WIL>
```

A;Cross-references: UNIPROT:O45732; EMBL:Z93387; PIDN:CAB07650.1; GSPDB:GN00023; CESP:T0
A;Experimental source: clone T02E9
C;Genetics:
A;Gene: CESP:T02E9.3
A;Map position: 5
A;Introns: 14/3; 281/2; 362/3; 405/1; 682/1; 724/1

Query Match 6.7%; Score 83.5; DB 2; Length 763;
Best Local Similarity 20.9%; Pred. No. 28;
Matches 36; Conservative 31; Mismatches 54; Indels 51; Gaps 6;

```
Qy         80 TDGSFVVHDIPSGSYVVEVV-------SPAYRFDPVRVDITSKGKMRARYVNYIKTSEVV 132
Db        435 SDGTSIMHKLSSGSSIAETVIAMLPKTSTLSKTDSHESSVSTEASQK------------- 481

Qy        133 RLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRR 192
Db        482 ----PL----LGPPTHHYTKKSQTQKEPRYSPSI-----PAPTFLMVPAMMAVNTPPATP 528

Qy        193 EMEQSMNMLNSNHELPDVSEFMTRLF-----------SSKSSGKSSSGSSKT 233
Db        529 NTKEAPTNCTSLLQVP-------RLFDCPSPCSVPSNSSHSSYTSASGSSDT 573
```

RESULT 12
S59990
phycobilisome anchor protein apcE - Synechocystis sp. (strain PCC 6714)
N;Alternate names: core-membrane linker protein
C;Species: Synechocystis sp.
A;Variety: PCC 6714
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S59990
R;DiMagno, L.; Haselkorn, R.
Plant Mol. Biol. 21, 835-845, 1993
A;Title: Isolation and characterization of the genes encoding allophycocyanin subunits a
A;Reference number: S33623; MUID:93222481; PMID:8467079
A;Accession: S59990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-896 <DIM>
A;Cross-references: UNIPROT:Q02907; EMBL:L02309; NID:g154474; PIDN:AAA69685.1; PID:g1544
A;Experimental source: PCC 6714
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
C;Genetics:
A;Gene: apcE

Query Match 6.7%; Score 83.5; DB 2; Length 896;
Best Local Similarity 22.0%; Pred. No. 35;
Matches 56; Conservative 33; Mismatches 87; Indels 79; Gaps 12;

```
Qy         18 SGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAAR---------- 66
Db         99 SSDSRNGSVTYAESNGGGGLFGGLRSVFSSTG-PIPPGFRP---INIARYGPSNMQKSLR 154

Qy         67 -----------VLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSK 115
Db        155 DMSWFLRYTTYAIVAGGPNIIVVNTRG-----------LKEVIENACSIDATIVRIQ-- 200

Qy        116 GKMRARYVNYIKTS----EVV-----------RLPYPLQMKSSG----------PPSYF- 149
Db        201 -EMRAASADYFRANAQAKEIVLQYFDILLSEFKAPTPANKVRQGPSNDIQGLELPQSYFN 259

Qy        150 --IKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHEL 207
Db        260 ASAKRQK-----YAMKPGLSALEKNAVIKAAYRQIF---ERDITKAYSQSISYLESQVRN 311

Qy        208 PDVS--EFMTRLFSS 220
Db        312 GDISMKEFVRRLAKS 326
```

RESULT 13
B49837
clathrin-associated protein AP50 homolog CEAP - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: B49837
R;Lee, J.; Jongeward, G.D.; Sternberg, P.W.
Genes Dev. 8, 60-73, 1994
A;Title: unc-101, a gene required for many aspects of Caenorhabditis elegans development
A;Reference number: A49837; MUID:94116859; PMID:8288128
A;Accession: B49837
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-441 <LEE>
A;Cross-references: UNIPROT:P35603; GB:L26290; NID:g451885; PIDN:AAA27981.1; PID:g451886
C;Superfamily: clathrin coat assembly protein AP50

Query Match 6.7%; Score 83; DB 2; Length 441;
Best Local Similarity 25.2%; Pred. No. 15;
Matches 40; Conservative 18; Mismatches 57; Indels 44; Gaps 6;

```
Qy         11 VLLLLLLSGDVQSSEVPGAAAEGSGGSGV-----GIGDRFKIEGRAVVPGVKPQDWISAA 65
Db        185 VNLLMNQQGQVLSAHVAGKVAMKSYLSGMPECKFGINDKITIEGKS-KPGSDDPNKASRA 243

Qy         66 RVLVDG--------------EEHVGFLKTDGSF------VVHDIPSGSYVVEVVSPAYRF 105
Db        244 AVAIDDCQFHQCVKLTKFETEHAISFIPPDGEYELMRYRTTKDIQLPFRVIPLVRE---- 299

Qy        106 DPVRVDITSKGKMRARYV-------NYIKTSEVVRLPYP 137
Db        300 -------VSRNKMEVKVVVKSNFKPSLLAQKLEVRIPTP 331
```

RESULT 14
C85017
probable CAAX prenyl proteinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85017
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85017
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <STO>
A;Cross-references: UNIPROT:Q9M139; GB:NC_001268; NID:g7267629; PIDN:CAB80941.1; GSPDB:GN
C;Genetics:
A;Gene: AT4g01320
A;Map position: 4

Query Match 6.7%; Score 83; DB 2; Length 459;
Best Local Similarity 22.8%; Pred. No. 16;
Matches 43; Conservative 36; Mismatches 80; Indels 30; Gaps 8;

```
Qy         55 GVKPQDWISAARVL----VDGEEHVGFLKTDGSFV--------VHDIPSGSYVVEVVSPA 102
Db         88 GILPWFWKMSGAVLPRLGLDPENEI--LHT-LSFLAGVMTWSQITDLPFSLYSTFVIESR 144

Qy        103 YRFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLM 162
Db        145 HGFNKQTIWMFIRDMIKGTFLSVILGPPIVAAIIFIVQK--GGPYLAI----YLWAFMFI 198

Qy        163 NPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKS 222
Db        199 LSLVMMTIYPVLIAPLFNKFTPLPDGDLREKIEK----LASSLKFP-----LKKLFVVDG 249

Qy        223 SGKSSSGSS 231
Db        250 STRSSHSNA 258
```

RESULT 15

AE1406
translation elongation factor G homolog fus [imported] - Listeria monocytogenes (strain
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1406
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-695 <GLA>
A;Cross-references: UNIPROT:Q8Y421; GB:NC_003210; PIDN:CAD00867.1; PID:g16412154; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: fus
C;Superfamily: translation elongation factor G; translation elongation factor Tu homolog

Query Match 6.7%; Score 83; DB 2; Length 695;
Best Local Similarity 26.6%; Pred. No. 28;
Matches 45; Conservative 19; Mismatches 45; Indels 60; Gaps 9;

```
Qy         22 QSSEVPGAAAEGSGGSG----VGI-------GDRFKIEGRAVVPGVKPQDWISAARVLVD 70
              :|::| |     ||| |    | |       |  |: |  |:| || |:::| | :  ::
Db        486 KSAQVEGKFVRQSGGRGQYGHVWIEFGPNEEGKGFEFE-NAIVGGVVPREYIPAVQAGLE 544

Qy         71 GEEHVGFLK----------TDGSFVVHDIPSGS------------------------- 93
              |    | |              |||:  ||: |
Db        545 GALDNGVLAGYPLIDIKAKLYDGSY--HDVDSNEMAFKVAASMALRNAAKKCDPVILEPM 602

Qy         94 YVVEVVSPAYRFDPVRVDITS-KGK---MRARYVNYIKTSEVVRLPYPL 138
              |||| |       :  :||| :|:   | ||        ::|||   ||
Db        603 MAVEVVIPEEYLGDIMGNITSRRGRVDGMEAR-----GNAQVVRAFVPL 646
```

Search completed: December 24, 2004, 20:22:54
Job time : 69 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2004, 20:14:19 ; Search time 76 Seconds
(without alignments)
1142.270 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 6

Total number of hits satisfying chosen parameters: 32788

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	242	100.0	242	3	AAB34724	Aab34724 Human sec
2	242	100.0	242	4	AAM23598	Aam23598 Human EST
3	242	100.0	242	4	AAU29217	Aau29217 Human PRO
4	242	100.0	242	4	AAB97078	Aab97078 Human hAR
5	242	100.0	242	4	AAB87593	Aab87593 Human PRO
6	242	100.0	242	5	ABG95918	Abg95918 Human sec
7	242	100.0	242	6	ABU58593	Abu58593 Human PRO
8	242	100.0	242	6	ABU88141	Abu88141 Novel hum
9	242	100.0	242	6	ABU84456	Abu84456 Human sec
10	242	100.0	242	6	ABR66330	Abr66330 Human sec
11	242	100.0	242	6	ABR65720	Abr65720 Human sec
12	242	100.0	242	6	ABU99660	Abu99660 Human sec
13	242	100.0	242	6	ABU82899	Abu82899 Human PRO
14	242	100.0	242	6	ABU90020	Abu90020 Novel hum
15	242	100.0	242	6	ABR68269	Abr68269 Human sec
16	242	100.0	242	6	ABJ37039	Abj37039 Human bre
17	242	100.0	242	6	ABU96322	Abu96322 Novel hum
18	242	100.0	242	6	ABU92753	Abu92753 Human sec
19	242	100.0	242	6	ABO08830	Abo08830 Human sec
20	242	100.0	242	6	ABO02882	Abo02882 Human sec
21	242	100.0	242	6	ABR75036	Abr75036 Human sec
22	242	100.0	242	6	ABR94798	Abr94798 Human sec
23	242	100.0	242	6	ABU85771	Abu85771 Human PRO
24	242	100.0	242	6	ABU98931	Abu98931 Novel hum
25	242	100.0	242	6	ABU98146	Abu98146 Novel hum
26	242	100.0	242	6	ABU91852	Abu91852 Novel hum
27	242	100.0	242	6	ABU89545	Abu89545 Human PRO
28	242	100.0	242	6	ABU86386	Abu86386 Human sec
29	242	100.0	242	6	ABU67599	Abu67599 Human sec
30	242	100.0	242	6	ABU80627	Abu80627 Human PRO
31	242	100.0	242	6	ABU90943	Abu90943 Novel hum
32	242	100.0	242	6	ABO34002	Abo34002 Human sec
33	242	100.0	242	6	ABR99545	Abr99545 Human sec
34	242	100.0	242	6	ABR98935	Abr98935 Human sec
35	242	100.0	242	6	ABO16458	Abo16458 Human sec
36	242	100.0	242	6	ABR92358	Abr92358 Human sec
37	242	100.0	242	6	ABO18999	Abo18999 Human sec
38	242	100.0	242	6	ABR78420	Abr78420 Human sec
39	242	100.0	242	6	ABU72019	Abu72019 Novel hum
40	242	100.0	242	6	ABU85156	Abu85156 Novel hum
41	242	100.0	242	6	ABO00295	Abo00295 Novel hum
42	242	100.0	242	6	ABO11627	Abo11627 Human sec
43	242	100.0	242	6	ABO02272	Abo02272 Human sec
44	242	100.0	242	6	ABU88846	Abu88846 Novel hum
45	242	100.0	242	6	ABU83541	Abu83541 Human sec

ALIGNMENTS

RESULT 1
AAB34724
ID AAB34724 standard; protein; 242 AA.
XX
AC AAB34724;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by DNA clone vo25 1.
XX
KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200055375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0149639P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.
DR N-PSDB; AAC59825.
XX
PT Novel proteins and polypeptides useful for the treatment of e.g multiple
PT sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer,
PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
XX
PS Claim 84; Page 437-438; 493pp; English.
XX
CC This invention relates to 59 human secreted proteins and the nucleotide
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC represent the proteins and their encoding nucleotide sequences, and

```
CC   sequences AAB34746-B34771 represent fragments of the proteins. Probes for
CC   the DNA sequences are represented by sequences AAC59847-C59596. The
CC   proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC   antiinflammatory, antianaemic, nootropic, antiparkinsonian,
CC   cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,
CC   antibacterial, virucide, and fungicide activity. The proteins and
CC   nucleotide sequences are useful as nutritional sources or supplements and
CC   in research. The proteins are useful for treating immune deficiency and
CC   disorders, which may be genetic or resulting from infections, autoimmune
CC   disorders such as multiple sclerosis, systemic lupus erythmatosus,
CC   rheumatoid arthritis, and for treating myeloid or lymphoid cell
CC   deficiencies such as anaemias by regulating haematopoiesis. The proteins
CC   are also useful in compositions for bone, cartilage, tendon, ligament
CC   and/or nerve tissue growth or regeneration, for wound healing, tissue
CC   repair and replacement and in the treatment of wounds, incisions and
CC   ulcers. Other uses include in the treatment of central and peripheral
CC   nervous system and neuropathies such as Alzheimer's and Parkinson's
CC   diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
CC   such as spinal cord disorders, head trauma and stroke. The proteins may
CC   also be used as a contraceptive, and for treating coagulation disorders
CC   such as haemophilias. The protein and nucleotide sequences with cadherin
CC   activity are useful for treating cancer. Other uses for the protein
CC   include for inhibiting the growth, infection or function of, or killing,
CC   infectious agents such as bacteria, virus, fungi and other parasites, for
CC   effecting bodily characteristics such as height, weight, hair colour,
CC   effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
CC   catabolism, anabolism, processing, utilization, storage or elimination of
CC   dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
CC   effecting behavioural characteristics, providing analgesic effects and
CC   for treating hyperproliferative disorders such as psoriasis
XX
SQ   Sequence 242 AA;

  Query Match             100.0%;  Score 242;  DB 3;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-225;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 2
AAM23598
ID   AAM23598 standard; protein; 242 AA.
XX
AC   AAM23598;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human EST encoded protein SEQ ID NO: 1123.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW   gene therapy; nutrition.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US002687.
XX
PR   25-JAN-2000; 2000US-00491404.
PR   17-JUL-2000; 2000US-00617746.
PR   03-AUG-2000; 2000US-00631451.
PR   15-SEP-2000; 2000US-00663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Qian XB,  Wang Z,  Chen R,  Asundi V;
PI   Cao Y,  Drmanac RA,  Zhang J,  Werhman T;
XX
DR   WPI; 2001-476164/51.
DR   N-PSDB; AAH98257.
XX
PT   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use.
XX
PS   Claim 20; Page 834-835; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a
CC   protein of the invention
XX
SQ   Sequence 242 AA;

  Query Match             100.0%;  Score 242;  DB 4;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-225;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 3
AAU29217
ID   AAU29217 standard; protein; 242 AA.
XX
AC   AAU29217;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #194.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
```

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS46118.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 11; Fig 388; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 242; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

RESULT 4
AAB97078
ID AAB97078 standard; protein; 242 AA.
XX
AC AAB97078;
XX
DT 01-AUG-2001 (first entry)
XX
DE Human hARP-20kDs protein.
XX
KW Human; actin associated protein compound subunit protein; hARP-20kDs;
KW hypothalamus.
XX
OS Homo sapiens.
XX
PN CN1281040-A.
XX
PD 24-JAN-2001.
XX
PF 27-JUN-2000; 2000CN-00116787.
XX
PR 27-JUN-2000; 2000CN-00116787.
XX
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI Xu X, Qian B, Yang Y;
XX
DR WPI; 2001-282650/30.
DR N-PSDB; AAH24361.
XX
PT New human actin associated protein compound subunit protein, its coding
PT sequence and preparing and detecting the protein and nucleic acid.
XX
PS Claim 2; Page 17; 18pp; Chinese.
XX
CC The present sequence is provided in a specification relating to a new

```
CC   human actin associated protein compound subunit protein (hARP)-20kDs
CC   expressed in human hypothalamus and its coding sequence. The process for
CC   preparing the protein and its nucleic acid sequence and the method for
CC   detecting hARP-20kDs nucleic acid sequence and polypeptide are also
CC   disclosed
XX
SQ   Sequence 242 AA;

  Query Match            100.0%;  Score 242;  DB 4;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-225;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 5
AAB87593
ID   AAB87593 standard; protein; 242 AA.
XX
AC   AAB87593;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1926.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92125.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 12; Fig 136; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping
XX
SQ   Sequence 242 AA;

  Query Match            100.0%;  Score 242;  DB 4;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-225;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 6
ABG95918
ID   ABG95918 standard; protein; 242 AA.
XX
AC   ABG95918;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human secreted/transmembrane protein PRO1926.
XX
KW   Human; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-00006867.
XX
PR   29-OCT-1997;   97US-0063435P.
PR   29-OCT-1997;   97US-0064215P.
PR   22-APR-1998;   98US-0082797P.
PR   29-APR-1998;   98US-0083495P.
PR   15-MAY-1998;   98US-0085579P.
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PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX

PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR N-PSDB; ABS74445.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 20; Fig 136; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 242; DB 5; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
Db 1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy 61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
Db 61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy 121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
Db 121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

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Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

RESULT 7
ABU58593
ID ABU58593 standard; protein; 242 AA.
XX
AC ABU58593;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #194.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
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PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
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PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.

PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
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PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
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Qy        241 RR 242
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Db        241 RR 242
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RESULT 8
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DT 07-JUL-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
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Query Match 100.0%; Score 242; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 RR 242
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Db        241 RR 242
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RESULT 9
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DT 02-AUG-2003 (first entry)
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XX
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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PD 13-FEB-2003.
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PF 21-JUN-2002; 2002US-00176756.
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Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 RR 242
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Db        241 RR 242
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RESULT 10
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AC ABR66330;
XX
DT 05-AUG-2003 (first entry)
XX
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
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Query Match 100.0%; Score 242; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 RR 242
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Db        241 RR 242
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DT 05-AUG-2003 (first entry)
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00188773.
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Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 RR 242
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Db        241 RR 242
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DT 09-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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OS Homo sapiens.
XX
PN US2003040070-A1.
XX

PD 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
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Query Match 100.0%; Score 242; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        241 RR 242
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RESULT 13
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ID ABU82899 standard; protein; 242 AA.
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DT 27-JUN-2003 (first entry)
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KW chromosome mapping; gene mapping; cytostatic.
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Query Match 100.0%; Score 242; DB 6; Length 242;
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Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
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Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242
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RESULT 14
ABU90020
ID ABU90020 standard; protein; 242 AA.
XX
AC ABU90020;
XX
DT 11-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926.
XX
KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
XX
OS Homo sapiens.
XX
PN US2003036147-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187741.
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Query Match 100.0%; Score 242; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
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Qy        241 RR 242
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Db        241 RR 242
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RESULT 15
ABR68269
ID ABR68269 standard; protein; 242 AA.
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AC ABR68269;
XX
DT 11-AUG-2003 (first entry)
XX
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174579.
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Query Match 100.0%; Score 242; DB 6; Length 242;
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Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

Search completed: December 24, 2004, 20:31:27
Job time : 79 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 24, 2004, 20:09:24 ; Search time 422 Seconds
(without alignments)
205.939 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 1242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1242	100.0	242	13	US-10-006-867-136	Sequence 136, App
2	1242	100.0	242	13	US-10-052-586-388	Sequence 388, App
3	1242	100.0	242	13	US-10-063-547-136	Sequence 136, App
4	1242	100.0	242	13	US-10-063-551-136	Sequence 136, App
5	1242	100.0	242	14	US-10-174-590-388	Sequence 388, App
6	1242	100.0	242	14	US-10-176-758-388	Sequence 388, App
7	1242	100.0	242	14	US-10-175-737-388	Sequence 388, App
8	1242	100.0	242	14	US-10-063-616-136	Sequence 136, App
9	1242	100.0	242	14	US-10-174-581-388	Sequence 388, App
10	1242	100.0	242	14	US-10-176-483-388	Sequence 388, App
11	1242	100.0	242	14	US-10-176-749-388	Sequence 388, App
12	1242	100.0	242	14	US-10-176-914-388	Sequence 388, App
13	1242	100.0	242	14	US-10-176-915-388	Sequence 388, App
14	1242	100.0	242	14	US-10-063-569-136	Sequence 136, App
15	1242	100.0	242	14	US-10-063-513-136	Sequence 136, App
16	1242	100.0	242	14	US-10-063-515-136	Sequence 136, App
17	1242	100.0	242	14	US-10-063-512-136	Sequence 136, App
18	1242	100.0	242	14	US-10-173-706-388	Sequence 388, App
19	1242	100.0	242	14	US-10-175-738-388	Sequence 388, App
20	1242	100.0	242	14	US-10-175-752-388	Sequence 388, App
21	1242	100.0	242	14	US-10-176-482-388	Sequence 388, App
22	1242	100.0	242	14	US-10-176-757-388	Sequence 388, App
23	1242	100.0	242	14	US-10-176-913-388	Sequence 388, App
24	1242	100.0	242	14	US-10-180-552-388	Sequence 388, App
25	1242	100.0	242	14	US-10-180-557-388	Sequence 388, App
26	1242	100.0	242	14	US-10-063-502-136	Sequence 136, App
27	1242	100.0	242	14	US-10-173-700-388	Sequence 388, App
28	1242	100.0	242	14	US-10-174-572-388	Sequence 388, App
29	1242	100.0	242	14	US-10-174-579-388	Sequence 388, App
30	1242	100.0	242	14	US-10-174-582-388	Sequence 388, App
31	1242	100.0	242	14	US-10-174-588-388	Sequence 388, App
32	1242	100.0	242	14	US-10-175-739-388	Sequence 388, App
33	1242	100.0	242	14	US-10-175-740-388	Sequence 388, App
34	1242	100.0	242	14	US-10-175-743-388	Sequence 388, App
35	1242	100.0	242	14	US-10-176-488-388	Sequence 388, App
36	1242	100.0	242	14	US-10-176-492-388	Sequence 388, App
37	1242	100.0	242	14	US-10-176-747-388	Sequence 388, App
38	1242	100.0	242	14	US-10-176-750-388	Sequence 388, App
39	1242	100.0	242	14	US-10-176-985-388	Sequence 388, App
40	1242	100.0	242	14	US-10-176-987-388	Sequence 388, App
41	1242	100.0	242	14	US-10-176-992-388	Sequence 388, App
42	1242	100.0	242	14	US-10-176-993-388	Sequence 388, App
43	1242	100.0	242	14	US-10-184-658-388	Sequence 388, App
44	1242	100.0	242	14	US-10-176-991-388	Sequence 388, App
45	1242	100.0	242	14	US-10-063-549-136	Sequence 136, App

ALIGNMENTS

RESULT 1
US-10-006-867-136
; Sequence 136, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-06-09
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; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 1242; DB 13; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.7e-119;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
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Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242
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RESULT 2
US-10-052-586-388
; Sequence 388, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1242; DB 13; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.7e-119;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
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RESULT 3
US-10-063-547-136
; Sequence 136, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547

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;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-547-136

  Query Match             100.0%;  Score 1242;  DB 13;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 4
US-10-063-551-136
; Sequence 136, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,551
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-551-136

  Query Match             100.0%;  Score 1242;  DB 13;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 5
US-10-174-590-388
; Sequence 388, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-174-590-388

  Query Match             100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 6
US-10-176-758-388
; Sequence 388, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
```

```
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-758-388

  Query Match            100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 7
US-10-175-737-388
; Sequence 388, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C50
;  CURRENT APPLICATION NUMBER: US/10/175,737
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-737-388

  Query Match            100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 8
US-10-063-616-136
; Sequence 136, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,616
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-616-136

  Query Match            100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
```

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
                ||
Db        241 RR 242


RESULT 9
US-10-174-581-388
; Sequence 388, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C41
;  CURRENT APPLICATION NUMBER: US/10/174,581
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063564
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063734
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063870
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066120
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/066466
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069425
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: 60/069870
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/068017
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/079786
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/080107
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080194
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080327
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/080333
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/081049
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081070
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081195
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081838
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082568
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082569
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082704
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083495
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083496
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083499
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083559
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/084366
;  PRIOR FILING DATE: 1998-05-05
;  PRIOR APPLICATION NUMBER: 60/084414
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/084639
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084640
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084643
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085573
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085580
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085582
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085700
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/086023
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/086392
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/086486
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;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087098
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 60/087208
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 60/087609
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/087759
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/087827
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;  PRIOR APPLICATION NUMBER: 60/088025
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088028
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088029
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;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088167
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/088202
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/088212
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/088217
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/088326
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088655
;  PRIOR FILING DATE: 1998-06-09
;  PRIOR APPLICATION NUMBER: 60/088722
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088738
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088740
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088811
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088824
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088825
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088826
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088861
;  PRIOR FILING DATE: 1998-06-11
;  PRIOR APPLICATION NUMBER: 60/088863
;  PRIOR FILING DATE: 1998-06-11
;  PRIOR APPLICATION NUMBER: 60/088876
;  PRIOR FILING DATE: 1998-06-11
;  PRIOR APPLICATION NUMBER: 60/089090
;  PRIOR FILING DATE: 1998-06-12
;  PRIOR APPLICATION NUMBER: 60/089105
;  PRIOR FILING DATE: 1998-06-12
;  PRIOR APPLICATION NUMBER: 60/089512
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089514
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089538
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089598
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089653

  Query Match           100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 10
US-10-176-483-388
; Sequence 388, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C68
;  CURRENT APPLICATION NUMBER: US/10/176,483
;  CURRENT FILING DATE:  2002-06-20
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-483-388

  Query Match           100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242


RESULT 11
US-10-176-749-388
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; Sequence 388, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C76
;  CURRENT APPLICATION NUMBER: US/10/176,749
;  CURRENT FILING DATE:  2002-06-20
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-749-388

  Query Match             100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 12
US-10-176-914-388
; Sequence 388, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C83
;  CURRENT APPLICATION NUMBER: US/10/176,914
;  CURRENT FILING DATE:  2002-06-20
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-914-388

  Query Match             100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242


RESULT 13
US-10-176-915-388
; Sequence 388, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C110
;  CURRENT APPLICATION NUMBER: US/10/176,915
;  CURRENT FILING DATE:  2002-06-21
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 388
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-915-388

  Query Match             100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 14
US-10-063-569-136
; Sequence 136, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,569
;  CURRENT FILING DATE:  2002-05-02
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-569-136

  Query Match            100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 15
US-10-063-513-136
; Sequence 136, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,513
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 136
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-513-136

  Query Match            100.0%;  Score 1242;  DB 14;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-119;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


Search completed: December 24, 2004, 20:30:03
Job time : 424 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2004, 17:53:58 ; Search time 287 Seconds
(without alignments)
302.483 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 1242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1242	100.0	242	3	AAB34724	Aab34724 Human sec
2	1242	100.0	242	4	AAM23598	Aam23598 Human EST
3	1242	100.0	242	4	AAU29217	Aau29217 Human PRO
4	1242	100.0	242	4	AAB97078	Aab97078 Human hAR
5	1242	100.0	242	4	AAB87593	Aab87593 Human PRO
6	1242	100.0	242	5	ABG95918	Abg95918 Human sec
7	1242	100.0	242	6	ABU58593	Abu58593 Human PRO
8	1242	100.0	242	6	ABU88141	Abu88141 Novel hum
9	1242	100.0	242	6	ABU84456	Abu84456 Human sec
10	1242	100.0	242	6	ABR66330	Abr66330 Human sec
11	1242	100.0	242	6	ABR65720	Abr65720 Human sec
12	1242	100.0	242	6	ABU99660	Abu99660 Human sec
13	1242	100.0	242	6	ABU82899	Abu82899 Human PRO
14	1242	100.0	242	6	ABU90020	Abu90020 Novel hum
15	1242	100.0	242	6	ABR68269	Abr68269 Human sec
16	1242	100.0	242	6	ABJ37039	Abj37039 Human bre
17	1242	100.0	242	6	ABU96322	Abu96322 Novel hum
18	1242	100.0	242	6	ABU92753	Abu92753 Human sec
19	1242	100.0	242	6	ABO08830	Abo08830 Human sec
20	1242	100.0	242	6	ABO02882	Abo02882 Human sec
21	1242	100.0	242	6	ABR75036	Abr75036 Human sec
22	1242	100.0	242	6	ABR94798	Abr94798 Human sec
23	1242	100.0	242	6	ABU85771	Abu85771 Human PRO
24	1242	100.0	242	6	ABU98931	Abu98931 Novel hum
25	1242	100.0	242	6	ABU98146	Abu98146 Novel hum
26	1242	100.0	242	6	ABU91852	Abu91852 Novel hum
27	1242	100.0	242	6	ABU89545	Abu89545 Human PRO
28	1242	100.0	242	6	ABU86386	Abu86386 Human sec
29	1242	100.0	242	6	ABU67599	Abu67599 Human sec
30	1242	100.0	242	6	ABU80627	Abu80627 Human PRO
31	1242	100.0	242	6	ABU90943	Abu90943 Novel hum
32	1242	100.0	242	6	ABO34002	Abo34002 Human sec
33	1242	100.0	242	6	ABR99545	Abr99545 Human sec
34	1242	100.0	242	6	ABR98935	Abr98935 Human sec
35	1242	100.0	242	6	ABO16458	Abo16458 Human sec
36	1242	100.0	242	6	ABR92358	Abr92358 Human sec
37	1242	100.0	242	6	ABO18999	Abo18999 Human sec
38	1242	100.0	242	6	ABR78420	Abr78420 Human sec
39	1242	100.0	242	6	ABU72019	Abu72019 Novel hum
40	1242	100.0	242	6	ABU85156	Abu85156 Novel hum
41	1242	100.0	242	6	ABO00295	Abo00295 Novel hum
42	1242	100.0	242	6	ABO11627	Abo11627 Human sec
43	1242	100.0	242	6	ABO02272	Abo02272 Human sec
44	1242	100.0	242	6	ABU88846	Abu88846 Novel hum
45	1242	100.0	242	6	ABU83541	Abu83541 Human sec

ALIGNMENTS

RESULT 1
AAB34724
ID AAB34724 standard; protein; 242 AA.
XX
AC AAB34724;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by DNA clone vo25 1.
XX
KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200055375-A1.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US007285.
XX
PR 17-MAR-1999; 99US-0124808P.
PR 17-MAR-1999; 99US-0124916P.
PR 17-AUG-1999; 99US-0149639P.
PR 01-OCT-1999; 99US-0157247P.
PR 29-NOV-1999; 99US-0167824P.
PR 15-FEB-2000; 2000US-0182711P.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-638211/61.
DR N-PSDB; AAC59825.
XX
PT Novel proteins and polypeptides useful for the treatment of e.g multiple
PT sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer,
PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
XX
PS Claim 84; Page 437-438; 493pp; English.
XX
CC This invention relates to 59 human secreted proteins and the nucleotide
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC represent the proteins and their encoding nucleotide sequences, and

CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for
CC the DNA sequences are represented by sequences AAC59847-C59596. The
CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC antiinflammatory, antianaemic, nootropic, antiparkinsonian,
CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,
CC antibacterial, virucide, and fungicide activity. The proteins and
CC nucleotide sequences are useful as nutritional sources or supplements and
CC in research. The proteins are useful for treating immune deficiency and
CC disorders, which may be genetic or resulting from infections, autoimmune
CC disorders such as multiple sclerosis, systemic lupus erythmatosus,
CC rheumatoid arthritis, and for treating myeloid or lymphoid cell
CC deficiencies such as anaemias by regulating haematopoiesis. The proteins
CC are also useful in compositions for bone, cartilage, tendon, ligament
CC and/or nerve tissue growth or regeneration, for wound healing, tissue
CC repair and replacement and in the treatment of wounds, incisions and
CC ulcers. Other uses include in the treatment of central and peripheral
CC nervous system and neuropathies such as Alzheimer's and Parkinson's
CC diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
CC such as spinal cord disorders, head trauma and stroke. The proteins may
CC also be used as a contraceptive, and for treating coagulation disorders
CC such as haemophilias. The protein and nucleotide sequences with cadherin
CC activity are useful for treating cancer. Other uses for the protein
CC include for inhibiting the growth, infection or function of, or killing,
CC infectious agents such as bacteria, virus, fungi and other parasites, for
CC effecting bodily characteristics such as height, weight, hair colour,
CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
CC catabolism, anabolism, processing, utilization, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
CC effecting behavioural characteristics, providing analgesic effects and
CC for treating hyperproliferative disorders such as psoriasis
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 1242; DB 3; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.6e-128;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

RESULT 2
AAM23598
ID AAM23598 standard; protein; 242 AA.
XX
AC AAM23598;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1123.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX

OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAH98257.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 834-835; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 1242; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.6e-128;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

RESULT 3
AAU29217
ID AAU29217 standard; protein; 242 AA.
XX
AC AAU29217;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #194.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS46118.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 11; Fig 388; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 1242; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.6e-128;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242
```

RESULT 4
AAB97078
ID AAB97078 standard; protein; 242 AA.
XX
AC AAB97078;
XX
DT 01-AUG-2001 (first entry)
XX
DE Human hARP-20kDs protein.
XX
KW Human; actin associated protein compound subunit protein; hARP-20kDs;
KW hypothalamus.
XX
OS Homo sapiens.
XX
PN CN1281040-A.
XX
PD 24-JAN-2001.
XX
PF 27-JUN-2000; 2000CN-00116787.
XX
PR 27-JUN-2000; 2000CN-00116787.
XX
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI Xu X, Qian B, Yang Y;
XX
DR WPI; 2001-282650/30.
DR N-PSDB; AAH24361.
XX
PT New human actin associated protein compound subunit protein, its coding
PT sequence and preparing and detecting the protein and nucleic acid.
XX
PS Claim 2; Page 17; 18pp; Chinese.
XX
CC The present sequence is provided in a specification relating to a new

```
CC   human actin associated protein compound subunit protein (hARP)-20kDs
CC   expressed in human hypothalamus and its coding sequence. The process for
CC   preparing the protein and its nucleic acid sequence and the method for
CC   detecting hARP-20kDs nucleic acid sequence and polypeptide are also
CC   disclosed
XX
SQ   Sequence 242 AA;

  Query Match           100.0%;  Score 1242;  DB 4;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-128;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 5
AAB87593
ID   AAB87593 standard; protein; 242 AA.
XX
AC   AAB87593;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1926.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92125.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 12; Fig 136; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping
XX
SQ   Sequence 242 AA;

  Query Match           100.0%;  Score 1242;  DB 4;  Length 242;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-128;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242


RESULT 6
ABG95918
ID   ABG95918 standard; protein; 242 AA.
XX
AC   ABG95918;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human secreted/transmembrane protein PRO1926.
XX
KW   Human; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-00006867.
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PR   29-OCT-1997;   97US-0063435P.
PR   29-OCT-1997;   97US-0064215P.
PR   22-APR-1998;   98US-0082797P.
PR   29-APR-1998;   98US-0083495P.
PR   15-MAY-1998;   98US-0085579P
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PR 02-JUN-1998; 98US-0087759P.
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PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
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PR 17-AUG-1998; 98US-0096757P.
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PR 16-SEP-1998; 98US-0100627P.
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PR 16-SEP-1998; 98WO-US019330.
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PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX

PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR N-PSDB; ABS74445.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 20; Fig 136; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 1242; DB 5; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.6e-128;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
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Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
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Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242
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RESULT 7
ABU58593
ID ABU58593 standard; protein; 242 AA.
XX
AC ABU58593;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #194.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
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PR 18-SEP-1997; 97US-0059263P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1242; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.6e-128;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
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Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
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Db        241 RR 242
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RESULT 8
ABU88141
ID ABU88141 standard; protein; 242 AA.
XX
AC ABU88141;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926.
XX
KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
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Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 RR 242
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Db        241 RR 242
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RESULT 9
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AC ABU84456;
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DT 02-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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OS Homo sapiens.
XX
PN US2003032112-A1.
XX
PD 13-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176756.
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Query Match 100.0%; Score 1242; DB 6; Length 242;
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Db        241 RR 242
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RESULT 10
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DT 05-AUG-2003 (first entry)
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
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OS Homo sapiens.
XX
PN US2003027278-A1.
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PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
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Qy        241 RR 242
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Db        241 RR 242
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RESULT 11
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AC ABR65720;
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DT 05-AUG-2003 (first entry)
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KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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Query Match 100.0%; Score 1242; DB 6; Length 242;
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Db        241 RR 242
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DT 09-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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OS Homo sapiens.
XX
PN US2003040070-A1.
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PD 27-FEB-2003.
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PF 27-JUN-2002; 2002US-00184627.
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Qy        241 RR 242
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Db        241 RR 242
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DT 27-JUN-2003 (first entry)
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KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KW chromosome mapping; gene mapping; cytostatic.
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OS Homo sapiens.
XX
PN US2003032113-A1.
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PD 13-FEB-2003.
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KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
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XX
PN US2003036147-A1.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00187741.
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KW antiarthritic; vulnerary; gene therapy.
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Query Match 100.0%; Score 1242; DB 6; Length 242;
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GenCore version 5.1.6

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Fgapop 6.0 , Fgapext 7.0
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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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59	1242	100.0	884	10	ADI01382	Adi01382 Novel hum
60	1242	100.0	884	10	ADI02077	Adi02077 Novel hum
61	1242	100.0	884	10	ADI03335	Adi03335 Novel hum
62	1242	100.0	884	10	ADI11522	Adi11522 Human PRO
63	1242	100.0	884	10	ADI02424	Adi02424 Novel hum
64	1242	100.0	884	10	ADI11862	Adi11862 Human PRO
65	1242	100.0	884	10	ADI05499	Adi05499 Novel hum
66	1242	100.0	884	10	ADH79571	Adh79571 Novel hum
67	1242	100.0	884	10	ADI19528	Adi19528 Novel hum
68	1242	100.0	884	10	ADI05329	Adi05329 Novel hum
69	1242	100.0	884	10	ADH79741	Adh79741 Novel hum
70	1242	100.0	884	10	ADI01567	Adi01567 Novel hum
71	1242	100.0	884	10	ADI01737	Adi01737 Novel hum
72	1242	100.0	884	10	ADI01907	Adi01907 Novel hum
73	1242	100.0	884	10	ADH79911	Adh79911 Novel hum
74	1242	100.0	884	10	ADI04729	Adi04729 Novel hum
75	1242	100.0	884	10	ADI02865	Adi02865 Novel hum
76	1242	100.0	884	10	ADH78184	Adh78184 Human PRO
77	1242	100.0	884	10	ADI25823	Adi25823 Novel hum
78	1242	100.0	884	10	ADI25993	Adi25993 Novel hum
79	1242	100.0	884	10	ADH98847	Adh98847 Novel hum

80	1242	100.0	884	10	ADH80088	Adh80088 Novel hum
81	1242	100.0	884	12	ADC52273	Adc52273 Novel hum
82	1242	100.0	884	12	ADH06705	Adh06705 Novel hum
83	1242	100.0	884	12	ADH06535	Adh06535 Novel hum
84	1242	100.0	884	12	ADG68956	Adg68956 Novel hum
85	1242	100.0	884	12	ADH27846	Adh27846 Novel hum
86	1242	100.0	884	12	ADH25187	Adh25187 Novel hum
87	1242	100.0	884	12	ADH33819	Adh33819 Human PRO
88	1242	100.0	884	12	ADH02462	Adh02462 Human PRO
89	1242	100.0	884	12	ADH08069	Adh08069 Novel hum
90	1242	100.0	884	12	ADG69466	Adg69466 Novel hum
91	1242	100.0	884	12	ADH39286	Adh39286 Novel hum
92	1242	100.0	884	12	ADG84027	Adg84027 Human PRO
93	1242	100.0	884	12	ADG85571	Adg85571 Novel hum
94	1242	100.0	884	12	ADH06365	Adh06365 Novel hum
95	1242	100.0	884	12	ADH30195	Adh30195 Novel hum
96	1242	100.0	884	12	ADH24507	Adh24507 Novel hum
97	1242	100.0	884	12	ADG69636	Adg69636 Novel hum
98	1242	100.0	884	12	ADH07899	Adh07899 Novel hum
99	1242	100.0	884	12	ADG85911	Adg85911 Novel hum
100	1242	100.0	884	12	ADH39457	Adh39457 Novel hum

ALIGNMENTS

RESULT 1
ABS74445
ID ABS74445 standard; cDNA; 884 BP.
XX
AC ABS74445;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1926.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR P-PSDB; ABG95918.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 2; Fig 135; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are

CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-743-136 (1-242) x ABS74445 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 2
ACA91231
ID ACA91231 standard; cDNA; 884 BP.
XX
AC ACA91231;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
DR P-PSDB; ABU90943.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX
PS Disclosure; Fig 135; 345pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its

```
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126        Length:         884
Score:                  1242.00         Matches:        242
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     8               Gaps:           0

US-10-063-743-136 (1-242) x ACA91231 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 3
ACA60430
ID   ACA60430 standard; cDNA; 884 BP.
XX
AC   ACA60430;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   Human; secreted and transmembrane polypeptide; gene;
KW   ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW   therapeutic agent screening; chromosome identification; tissue typing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003018183-A1.
XX
PD   23-JAN-2003.
XX
PF   01-MAY-2002; 2002US-00063512.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-330984/31.
DR   P-PSDB; ABU72019.
XX
PT   New secreted and transmembrane PRO polypeptides and nucleic acid
PT   molecules encoding the polypeptides, useful in gene therapy or preparing
PT   a medicament for treating a condition that is responsive to the PRO
PT   polypeptide or antibody.
XX
PS   Disclosure; Fig 135; 409pp; English.
XX
CC   The invention describes novel isolated PRO polypeptides. The PRO
CC   polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC   for treating a condition that is responsive to the PRO polypeptide or
CC   antibody. The PRO nuclectide sequences may be used as hybridisation
CC   probes in chromosome and gene mapping, or in generating antisense RNA and
CC   DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC   assays to identify other proteins or molecules involved in binding
CC   reaction, to generate transgenic animals or knockout animals, which in
CC   turn are useful in the development and screening of therapeutically
CC   useful reagents, for chromosome identification, and tissue typing. The
CC   PRO polypeptides and nucleic acid molecules are also useful in gene
CC   therapy, and as molecular weight markers for protein electrophoresis
CC   purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC   PRO, or for the affinity purification of PRO from recombinant cell
CC   culture or natural sources. This sequence encodes a novel human secreted
CC   and transmembrane PRO poypeptide
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126        Length:         884
Score:                  1242.00         Matches:        242
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     8               Gaps:           0

US-10-063-743-136 (1-242) x ACA60430 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 4
ACA58877
ID ACA58877 standard; cDNA; 884 BP.
XX
AC ACA58877;
XX
DT 10-JUN-2003 (first entry)
XX
DE cDNA encoding human secreted polypeptide PRO1926.
XX
KW Human; ss; gene; gene therapy; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003013855-A1.
XX
PD 16-JAN-2003.
XX
PF 03-MAY-2002; 2002US-00063616.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330485/31.
DR P-PSDB; ABU71573.
XX
PT New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
PS Example 4; Page 208; 406pp; English.
XX
CC The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-063-743-136 (1-242) x ACA58877 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy          21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy          41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy          61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy          81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy         101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy         121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy         141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy         161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy         181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy         201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy         221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy         241 ArgArg 242
                ||||||
Db         744 AGGAGG 749
```

RESULT 5
ACA63440
ID ACA63440 standard; cDNA; 884 BP.
XX
AC ACA63440;
XX
DT 13-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #68.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003023042-A1.
XX
PD 30-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063502.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-331484/31.
DR P-PSDB; ABU72176.
XX
PT Novel monoclonal antibody that binds to secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and also
PT for treating conditions responsive to the antibody.
XX
PS Disclosure; Fig 135; 408pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ACA63373-ACA63456 represent cDNA sequences encoding the human PRO
CC polypeptides of the invention
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-063-743-136 (1-242) x ACA63440 (1-884)

```
Qy           1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy          21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy          41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy          61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy          81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy         101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy         121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy         141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy         161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563
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```
Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 6
ACH03643
ID ACH03643 standard; cDNA; 884 BP.
XX
AC ACH03643;
XX
DT 26-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 1926 cDNA.
XX
KW Human; ss; tumour; cancer; tissue typing; gene.
XX
OS Homo sapiens.
XX
PN US2003018172-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063513.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-479475/45.
DR P-PSDB; ABO44306.
XX
PT Isolated antibody specifically binding a PRO polypeptide, useful for the
PT diagnosis and treatment of disorders with the aberrant expression or
PT activity of the PRO polypeptide, such as tumor conditions and cancer.
XX
PS Disclosure; Fig 135; 409pp; English.
XX
CC The invention relates to an antibody that binds to a fully defined PRO
CC polypeptide. The antibody is useful for the diagnosis, prevention and/or
CC treatment of disorders associated with the aberrant expression or
CC activity of the PRO polypeptide, such as tumour conditions and cancer.
CC They can also be used to generate transgenic or knockout animals useful
CC in the development and screening of therapeutically useful reagents. The
CC PRO polypeptides and encoding nucleic acids can be used as molecular
CC weight markers for protein electrophoresis, chromosome identification and
CC tissue typing. The antibodies may be used in various diagnostic,
CC competitive binding and/or immunoprecipitation assays. The present
CC sequence represents cDNA encoding a human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-063-743-136 (1-242) x ACH03643 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 7
ADB17380
ID ADB17380 standard; cDNA; 884 BP.
XX
AC ADB17380;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cDNA clone (SeqID 135) encoding the transmembrane PRO protein.
XX
KW ss; gene; PRO; transmembrane; immunoconjugate; cytotoxic; gene therapy;
KW cytostatic; cancer; human.
XX
OS Homo sapiens.
XX
PN US2003050465-A1.

```
XX
PD   13-MAR-2003.
XX
PF   26-AUG-2002; 2002US-00227693.
XX
PR   10-AUG-1998;   98US-0096012P.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   24-AUG-2000; 2000WO-US023328.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-521821/49.
DR   P-PSDB; ADB17381.
XX
PT   New PRO nucleic acid, useful for manufacturing a medicament for
PT   diagnosing or treating tumor or for tissue typing.
XX
PS   Claim 2; Fig 135; 406pp; English.
XX
CC   This invention relates to a novel isolated and secreted PRO polypeptide.
CC   PRO is a transmembrane protein involved in the formation, differentiation
CC   and maintenance of multicellular organisms, and more particularly the
CC   proliferation, differentiation and migration of individual cells. The
CC   invention describes screening compounds to identify PRO polypeptide
CC   agonists and antagonists, anti-PRO antibodies, and immunoconjugates
CC   comprising an antibody conjugated to a cytotoxic agent. Specifically, the
CC   heterologous protein of the chimeric polypeptide is an epitope tag or an
CC   Fc region of an immunoglobulin. Through the use of gene therapy, the PRO
CC   polypeptide is useful for preparing cytostatic compositions for
CC   diagnosing or treating cancer. The polypeptide is also useful as a
CC   molecular weight marker for protein electrophoresis purposes. This
CC   polynucleotide sequence is a native cDNA clone that encodes human PRO
CC   polypeptide, found in the cDNA library of the invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:         884
Score:                    1242.00         Matches:        242
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       9               Gaps:           0

US-10-063-743-136 (1-242) x ADB17380 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 8
ADB68387
ID   ADB68387 standard; cDNA; 884 BP.
XX
AC   ADB68387;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human PRO1926 cDNA.
XX
KW   PRO; cytostatic; cancer; diabetes; hyperinsulinaemia; hypoinsulinaemia;
KW   sports-related joint problem; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; tissue typing; gene therapy; transgenic; human; ss;
KW   gene.
XX
OS   Homo sapiens.
XX
PN   US2003065161-A1.
XX
PD   03-APR-2003.
XX
PF   03-MAY-2002; 2002US-00063594.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-531738/50.
DR   P-PSDB; ADB68388.
XX
PT   Novel secreted and transmembrane polypeptide, designated PRO1270, useful
PT   for therapeutic and diagnostic purposes, for tissue typing and
PT   identifying modulators of therapeutic use.
XX
PS   Example 4; Fig 135; 413pp; English.
XX
CC   The invention relates to a novel isolated PRO polypeptide. The
CC   polypeptide of the invention demonstrates cytostatic activity and may be
CC   useful during the preparation of a composition for diagnosing or treating
CC   cancer, diabetes, h
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CC   joint problems, including articular cartilage defects, osteoarthritis and
CC   rheumatoid arthritis. Furthermore, the polypeptides may be utilised
CC   during tissue typing, gene therapy and the production of transgenic
CC   animals. The current sequence is that of the human PRO cDNA of the
CC   invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:         884
Score:                    1242.00         Matches:        242
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       10              Gaps:           0

US-10-063-743-136 (1-242) x ADB68387 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 9
ADB91011
ID   ADB91011 standard; cDNA; 884 BP.
XX
AC   ADB91011;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003083473-A1.
XX
PD   01-MAY-2003.
XX
PF   03-MAY-2002; 2002US-00063595.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-786922/74.
DR   P-PSDB; ADB91012.
XX
PT   New antibody that binds a secreted and transmembrane polypeptide (PRO)
PT   for treating cancer and for diagnostic assays and affinity purification
PT   of PRO.
XX
PS   Disclosure; Fig 135; 408pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:         884
Score:                    1242.00         Matches:        242
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       10              Gaps:           0

US-10-063-743-136 (1-242) x ADB91011 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263
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Qy          81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy         101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy         121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy         141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy         161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy         181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy         201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy         221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy         241 ArgArg 242
               ||||||
Db         744 AGGAGG 749
```

RESULT 10
ADC52463
ID ADC52463 standard; cDNA; 884 BP.
XX
AC ADC52463;
XX
DT 18-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003138882-A1.
XX
PD 24-JUL-2003.
XX
PF 08-MAY-2002; 2002US-00063735.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-829699/77.
DR P-PSDB; ADC52464.
XX
PT Novel isolated secreted and transmembrane PRO1774 cDNA sequence, used as
PT hybridization probes, and useful for diagnosing rectal tumors.
XX
PS Disclosure; SEQ ID NO 135; 410pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADC52463 (1-884)

```
Qy           1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy          21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy          41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy          61 TrpIleSerAlaAlaArgVal
               |||||||||||||||||||||
Db         204 TGGATCTCTGCTGCCAGGGTG
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Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100

Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120

Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140

Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160

Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180

Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200

Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220

Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240

Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242

Db        744 AGGAGG 749
```

RESULT 11
ADD36139
ID   ADD36139 standard; cDNA; 884 BP.
XX
AC   ADD36139;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003105298-A1.
XX
PD   05-JUN-2003.
XX
PF   03-MAY-2002; 2002US-00063580.
XX
PR   16-JUN-1998;   98US-0089514P.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   24-AUG-2000; 2000WO-US023328.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2003-829362/77.
DR   P-PSDB; ADD36140.

XX
PT   New antibody that binds to a secreted and transmembrane polypeptide (PRO)
PT   useful in diagnostic assays for PRO and as a PRO agonist or antagonist.
XX
PS   Disclosure; Fig 135; 408pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADD36139 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20

Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40

Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60

Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80

Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100

Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120

Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140

Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160

Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180

Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200

Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220

Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683
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Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 12
ADG01140
ID   ADG01140 standard; cDNA; 884 BP.
XX
AC   ADG01140;
XX
DT   26-FEB-2004 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003078387-A1.
XX
PD   24-APR-2003.
XX
PF   03-MAY-2002; 2002US-00063599.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2003-743855/70.
DR   P-PSDB; ADG01141.
XX
PT   New antibody that binds to PRO polypeptides, useful for the development
PT   and screening of therapeutically useful reagents, for chromosome
PT   identification, and for tissue typing.
XX
PS   Disclosure; Fig 135; 387pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADG01140 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
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```

```
Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 13
ADG08693
ID   ADG08693 standard; cDNA; 884 BP.
XX
AC   ADG08693;
XX
DT   26-FEB-2004 (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003180793-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063546.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.

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PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-787560/74.
DR   P-PSDB; ADG08694.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 562pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:          884
Score:                    1242.00         Matches:         242
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       10              Gaps:            0

US-10-063-743-136 (1-242) x ADG08693 (1-884)
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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

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RESULT 14
ADF95314
ID   ADF95314 standard; cDNA; 884 BP.
XX
AC   ADF95314;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003180795-A1.
XX
PD   25-SEP-2003.
XX
PF   07-MAY-2002; 2002US-00063662.
XX
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PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854260.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-787562/74.
DR   P-PSDB; ADF95315.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 562pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126      Length:         884
Score:                  1242.00       Matches:        242
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     10            Gaps:           0

US-10-063-743-136 (1-242) x ADF95314 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
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Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 15
ADH24167
ID   ADH24167 standard; cDNA; 884 BP.
XX
AC   ADH24167;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   antiarthritic; antidiabetic; cytostatic; vulnerary; hyperglycaemic;
KW   hypoglycaemic; antibody therapy; PRO; secreted and transmembrane;
KW   bone disorder; cartilage disorder; sports injury; arthritis;
KW   glucose uptake; skeletal muscle; diabetes; hyper-insulinaemia;
KW   hypo-insulinaemia; pericyte-associated tumour; wound healing; cancer;
KW   chromosome identification; gene therapy; gene; ss; human.
XX
OS   Homo sapiens.
```

XX
PN US2003180918-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063722.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-830993/77.
DR P-PSDB; ADH24168.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide comprising the 642 amino acid sequence (S1) defined in the
CC specification. The PRO polypeptides are useful for treating various bone
CC and/or cartilage disorders, for example, sports injuries and arthritis.
CC They are also useful in the therapeutic treatment of disorders where
CC either the stimulation or inhibition of glucose uptake by skeletal muscle
CC would be beneficial, for example, diabetes or hyper- or hypo-
CC insulinaemia. They are also useful for treating pericyte-associated
CC tumours and in wound healing. The anti-PRO antibody is useful for the
CC preparation of a medicament useful in the treatment of cancer. The PRO
CC polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a secreted and
CC transmembrane PRO protein.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH24167 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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RESULT 16
ADH34193
ID ADH34193 standard; cDNA; 884 BP.
XX
AC ADH34193;
XX
DT 11-MAR-2004 (first entry)

XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003180858-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063730.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-778508/73.
DR P-PSDB; ADH34194.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in molecular biology, chromosome and gene mapping, in generating
PT antisense RNA and DNA, in various diagnostic assays and in gene therapy.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH34193 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 17
ADH30026
ID ADH30026 standard; cDNA; 884 BP.
XX

AC ADH30026;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003180859-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063734.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-778509/73.
DR P-PSDB; ADH30027.
XX
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX
PS Disclosure; SEQ ID NO 135; 398pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH30026 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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RESULT 18

ADH23997
ID ADH23997 standard; cDNA; 884 BP.
XX
AC ADH23997;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW antiarthritic; antidiabetic; cytostatic; vulnerary; hyperglycaemic;
KW hypoglycaemic; antibody therapy; PRO; secreted and transmembrane;
KW bone disorder; cartilage disorder; sports injury; arthritis;
KW glucose uptake; skeletal muscle; diabetes; hyper-insulinaemia;
KW hypo-insulinaemia; pericyte-associated tumour; wound healing; cancer;
KW chromosome identification; gene therapy; gene; ss; human.
XX
OS Homo sapiens.
XX
PN US2003180919-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063726.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-830994/77.
DR P-PSDB; ADH23998.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide comprising the 642 amino acid sequence (S1) defined in the
CC specification. The PRO polypeptides are useful for treating various bone
CC and/or cartilage disorders, for example, sports injuries and arthritis.
CC They are also useful in the therapeutic treatment of disorders where
CC either the stimulation or inhibition of glucose uptake by skeletal muscle
CC would be beneficial, for example, diabetes or hyper- or hypo-
CC insulinaemia. They are also useful for treating pericyte-associated
CC tumours and in wound healing. The anti-PRO antibody is useful for the
CC preparation of a medicament useful in the treatment of cancer. The PRO
CC polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a secreted and
CC transmembrane PRO protein.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH23997 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 19
ADG85401
ID   ADG85401 standard; cDNA; 884 BP.
XX
AC   ADG85401;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003180904-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063565.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-830990/77.
DR   P-PSDB; ADG85402.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126      Length:          884
Score:                    1242.00       Matches:         242
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0

US-10-063-743-136 (1-242) x ADG85401 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623
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```
Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 20
ADH24677
ID ADH24677 standard; cDNA; 884 BP.
XX
AC ADH24677;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW antiarthritic; antidiabetic; cytostatic; vulnerary; hyperglycaemic;
KW hypoglycaemic; antibody therapy; PRO; secreted and transmembrane;
KW bone disorder; cartilage disorder; sports injury; arthritis;
KW glucose uptake; skeletal muscle; diabetes; hyper-insulinaemia;
KW hypo-insulinaemia; pericyte-associated tumour; wound healing; cancer;
KW chromosome identification; gene therapy; gene; ss; human.
XX
OS Homo sapiens.
XX
PN US2003180907-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063610.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-787563/74.
DR P-PSDB; ADH24678.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 563pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide comprising the 642 amino acid sequence (S1) defined in the
CC specification. The PRO polypeptides are useful for treating various bone
CC and/or cartilage disorders, for example, sports injuries and arthritis.
CC They are also useful in the therapeutic treatment of disorders where
CC either the stimulation or inhibition of glucose uptake by skeletal muscle
CC would be beneficial, for example, diabetes or hyper- or hypo-
CC insulinaemia. They are also useful for treating pericyte-associated
CC tumours and in wound healing. The anti-PRO antibody is useful for the
CC preparation of a medicament useful in the treatment of cancer. The PRO
CC polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a secreted and
CC transmembrane PRO protein.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH24677 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
```

```
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180

Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200

Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220

Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240

Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242

Db        744 AGGAGG 749
```

RESULT 21
ADH37533
ID ADH37533 standard; cDNA; 884 BP.
XX
AC ADH37533;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human secreted and transmembrane protein PRO1926 cDNA.
XX
KW PRO; cytostatic; antidiabetic; antiarthritic; osteopathic; antirheumatic;
KW secreted and transmembrane polypeptide; cancer; gene therapy; ss; gene;
KW human.
XX
OS Homo sapiens.
XX
PN US2003181646-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063607.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-787566/74.
DR P-PSDB; ADH37534.
XX
PT New secreted and transmembrane PRO polypeptides useful in preparing a
PT medicament for treating a condition that is responsive to the PRO
PT polypeptide e.g. diabetes.
XX
PS Example 4; SEQ ID NO 135; 397pp; English.
XX
CC This invention describes novel human PRO polypeptides and the
CC polynucleotides encoding them which have cytostatic, antidiabetic,
CC antiarthritic, osteopathic and antirheumatic activity. Specifically
CC claimed are secreted and transmembrane polypeptides, e.g. PRO180, PRO218,
CC PRO263, PRO295, PRO874, PRO300, PRO1864, PRO1282, PRO1063 or PRO1773
CC polypeptide. The PRO polypeptides or anti-PRO antibodies are useful for
CC preparing a medicament for treating a condition that is responsive to the
CC PRO polypeptide or anti-PRO antibody e.g. cancer, diabetes,
CC osteoarthritis or rheumatoid arthritis. PRO nucleotide sequences may be
CC used as hybridisation probes in chromosome and gene mapping or in
CC generating antisense RNA and DNA. The PRO nucleic acids are also useful
CC in preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, in generating transgenic animals
CC or knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO, or for the affinity purification of
CC PRO from recombinant cell culture or natural sources. This sequence
CC encodes a PRO polypeptide described in the disclosure of the invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH37533 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20

Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40

Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60

Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80

Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263
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```
Qy          81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy         101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy         121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy         141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy         161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy         181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy         201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy         221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy         241 ArgArg 242
               ||||||
Db         744 AGGAGG 749
```

RESULT 22
ADH02122
ID ADH02122 standard; cDNA; 884 BP.
XX
AC ADH02122;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PRO polynucleotide #68.
XX
KW Human; PRO; gene; ss; tumour necrosis factor-alpha; TNF-alpha; blood;
KW chondrocyte cell; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003180837-A1.
XX
PD 25-SEP-2003.
XX
PF 01-MAY-2002; 2002US-00063510.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-802875/75.
DR P-PSDB; ADH02123.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to an antibody
CC that specifically binds to the polypeptide, a method for stimulating the
CC release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a
CC method for stimulating proliferation or differentiation of chondrocyte
CC cells and a method for detecting the presence of a tumour in a mammal
CC comprising comparing the level of expression of any PRO polypeptide,
CC given in the specification, in a test sample of cells taken from the
CC mammal with a control sample of normal cells of the same cell type, where
CC a higher level of expression of the PRO polypeptide in the test sample as
CC compared to the control sample indicates the presence of a tumour in the
CC mammal. The polynucleotides are useful as hybridisation probes in
CC chromosome and gene mapping or in generating antisense RNA and DNA, for
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reactions, to generate transgenic animals
CC or knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification and in tissue typing. The PRO polypeptides and
CC polynucleotides are also useful in gene therapy and as molecular weight
CC markers for protein electrophoresis. The anti-PRO antibodies may be used
CC in diagnostic assays for PRO or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. This sequence represents a
CC human PRO polynucleotide of the invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH02122 (1-884)

```
Qy           1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
                 ||||||
Db        744 AGGAGG 749
```

RESULT 23
ADH37703
ID ADH37703 standard; cDNA; 884 BP.
XX
AC ADH37703;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human secreted and transmembrane protein PRO1926 cDNA.
XX
KW PRO; cytostatic; antidiabetic; antiarthritic; osteopathic; antirheumatic;
KW secreted and transmembrane polypeptide; cancer; gene therapy; ss; gene;
KW human.
XX
OS Homo sapiens.
XX
PN US2003181648-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063615.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-787567/74.
DR P-PSDB; ADH37704.
XX
PT New antibody that binds to a PRO polypeptide, useful in diagnostic assays
PT for PRO, or in preparing a medicament for treating a condition that is
PT responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer or
PT diabetes.
XX
PS Example 4; SEQ ID NO 135; 396pp; English.
XX
CC This invention describes novel human PRO polypeptides and the
CC polynucleotides encoding them which have cytostatic, antidiabetic,
CC antiarthritic, osteopathic and antirheumatic activity. Specifically
CC claimed are secreted and transmembrane polypeptides, e.g. PRO180, PRO218,
CC PRO263, PRO295, PRO874, PRO300, PRO1864, PRO1282, PRO1063 or PRO1773
CC polypeptide. The PRO polypeptides or anti-PRO antibodies are useful for
CC preparing a medicament for treating a condition that is responsive to the
CC PRO polypeptide or anti-PRO antibody e.g. cancer, diabetes,
CC osteoarthritis or rheumatoid arthritis. PRO nucleotide sequences may be
CC used as hybridisation probes in chromosome and gene mapping or in
CC generating antisense RNA and DNA. The PRO nucleic acids are also useful
CC in preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, in generating transgenic animals
CC or knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO, or for the affinity purification of
CC PRO from recombinant cell culture or natural sources. This sequence

```
CC   encodes a PRO polypeptide described in the disclosure of the invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126      Length:          884
Score:                  1242.00       Matches:         242
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     10            Gaps:            0

US-10-063-743-136 (1-242) x ADH37703 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 24
ADG85741
ID   ADG85741 standard; cDNA; 884 BP.
XX
AC   ADG85741;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003180905-A1.
XX
PD   25-SEP-2003.
XX
PF   03-MAY-2002; 2002US-00063577.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-802877/75.
DR   P-PSDB; ADG85742.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 563pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
```

CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADG85741 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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RESULT 25
ADH24337
ID ADH24337 standard; cDNA; 884 BP.
XX
AC ADH24337;

XX
DT 11-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW antiarthritic; antidiabetic; cytostatic; vulnerary; hyperglycaemic;
KW hypoglycaemic; antibody therapy; PRO; secreted and transmembrane;
KW bone disorder; cartilage disorder; sports injury; arthritis;
KW glucose uptake; skeletal muscle; diabetes; hyper-insulinaemia;
KW hypo-insulinaemia; pericyte-associated tumour; wound healing; cancer;
KW chromosome identification; gene therapy; gene; ss; human.
XX
OS Homo sapiens.
XX
PN US2003180914-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063715.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-830992/77.
DR P-PSDB; ADH24338.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide comprising the 642 amino acid sequence (S1) defined in the

```
CC   specification. The PRO polypeptides are useful for treating various bone
CC   and/or cartilage disorders, for example, sports injuries and arthritis.
CC   They are also useful in the therapeutic treatment of disorders where
CC   either the stimulation or inhibition of glucose uptake by skeletal muscle
CC   would be beneficial, for example, diabetes or hyper- or hypo-
CC   insulinaemia. They are also useful for treating pericyte-associated
CC   tumours and in wound healing. The anti-PRO antibody is useful for the
CC   preparation of a medicament useful in the treatment of cancer. The PRO
CC   polypeptides are also useful as molecular weight markers, or for
CC   chromosome identification. The PRO genes are useful as hybridisation
CC   probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC   The PRO genes may also be used in gene therapy, particularly for
CC   replacing a defective gene. This sequence encodes a secreted and
CC   transmembrane PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126      Length:          884
Score:                  1242.00       Matches:         242
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     10            Gaps:            0

US-10-063-743-136 (1-242) x ADH24337 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 26
ADH38631
ID   ADH38631 standard; cDNA; 884 BP.
XX
AC   ADH38631;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   human; PRO; membrane bound protein; membrane bound receptor;
KW   cell proliferation; cell migration; cell differentiation;
KW   mitogenic factor; survival factor; cytotoxic factor;
KW   differentiation factor; neuropeptide; hormone; cell receptor;
KW   receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS   Homo sapiens.
XX
PN   US2003181643-A1.
XX
PD   25-SEP-2003.
XX
PF   03-MAY-2002; 2002US-00063596.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
```

DR WPI; 2003-787565/74.
DR P-PSDB; ADH38632.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules, useful in gene therapy or preparing a medicament for treating
PT a condition that is responsive to the PRO polypeptide or anti-PRO
PT antibody, e.g. diabetes.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH38631 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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RESULT 27
ADG83752
ID ADG83752 standard; cDNA; 884 BP.
XX
AC ADG83752;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PRO polynucleotide #68.
XX
KW Human; PRO; gene; ss; cancer; affinity purification; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003180794-A1.
XX
PD 25-SEP-2003.
XX
PF 02-MAY-2002; 2002US-00063564.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.

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PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2003-787561/74.
DR   P-PSDB; ADG83753.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC   The invention relates to an antibody that binds to a human PRO
CC   polypeptide. The invention also relates to human PRO polynucleotides
CC   encoding the PRO polypeptides of the invention. The antibody is
CC   preferably a monoclonal or humanised antibody, or an antibody fragment,
CC   and is used to treat cancer. The anti-PRO antibody can be used in
CC   diagnostic assays, e.g. for detecting PRO expression in specific cells,
CC   tissues or serum. The anti-PRO antibodies are also useful for the
CC   affinity purification of PRO from recombinant cell culture or natural
CC   sources. This sequence represents a human PRO polynucleotide of the
CC   invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126        Length:         884
Score:                  1242.00         Matches:        242
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-063-743-136 (1-242) x ADG83752 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 28
ADH29560
ID   ADH29560 standard; cDNA; 884 BP.
XX
AC   ADH29560;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003180860-A1.
XX
PD   25-SEP-2003.
XX
PF   08-MAY-2002; 2002US-00063736.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520
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PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-830989/77.
DR P-PSDB; ADH29561.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC The invention describes an antibody that specifically binds to a PRO
CC polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH29560 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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RESULT 29
ADH27676
ID ADH27676 standard; cDNA; 884 BP.
XX
AC ADH27676;
XX
DT 11-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003180906-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063591.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.

```
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2003-830991/77.
DR   P-PSDB; ADH27677.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 398pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
CC   diagnostics, biosensors and bioreactors. The antibody is also used for
CC   affinity purification of PRO polypeptides from recombinant cell culture
CC   or natural sources. The antibody, PRO polypeptide, or its agonists or
CC   antagonists, may be used for preparing a medicament for diagnosing or
CC   treating a condition responsive to the antibody, PRO polypeptide, or its
CC   agonists or antagonists. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:          884
Score:                    1242.00         Matches:         242
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       10              Gaps:            0

US-10-063-743-136 (1-242) x ADH27676 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 30
ADH37873
ID   ADH37873 standard; cDNA; 884 BP.
XX
AC   ADH37873;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   PRO; cytostatic; antidiabetic; antiarthritic; osteopathic; antirheumatic;
KW   secreted and transmembrane polypeptide; cancer; gene therapy; ss; gene;
KW   human.
XX
OS   Homo sapiens.
XX
PN   US2003181647-A1.
XX
PD   25-SEP-2003.
XX
PF   03-MAY-2002; 2002US-00063612.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-802901/75.
DR P-PSDB; ADH37874.
XX
PT New secreted and transmembrane PRO polypeptide, useful for preparing a
PT medicament for treating a condition that is responsive to the PRO
PT polypeptide e.g. diabetes.
XX
PS Example 4; SEQ ID NO 135; 397pp; English.
XX
CC This invention describes novel human PRO polypeptides and the
CC polynucleotides encoding them which have cytostatic, antidiabetic,
CC antiarthritic, osteopathic and antirheumatic activity. Specifically
CC claimed are secreted and transmembrane polypeptides, e.g. PRO180, PRO218,
CC PRO263, PRO295, PRO874, PRO300, PRO1864, PRO1282, PRO1063 or PRO1773
CC polypeptide. The PRO polypeptides or anti-PRO antibodies are useful for
CC preparing a medicament for treating a condition that is responsive to the
CC PRO polypeptide or anti-PRO antibody e.g. cancer, diabetes,
CC osteoarthritis or rheumatoid arthritis. PRO nucleotide sequences may be
CC used as hybridisation probes in chromosome and gene mapping or in
CC generating antisense RNA and DNA. The PRO nucleic acids are also useful
CC in preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, in generating transgenic animals
CC or knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO, or for the affinity purification of
CC PRO from recombinant cell culture or natural sources. This sequence
CC encodes a PRO polypeptide described in the disclosure of the invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH37873 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 31
ADH38050
ID ADH38050 standard; cDNA; 884 BP.
XX
AC ADH38050;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human secreted and transmembrane protein PRO1926 cDNA.
XX
KW PRO; cytostatic; antidiabetic; antiarthritic; osteopathic; antirheumatic;
KW secreted and transmembrane polypeptide; cancer; gene therapy; ss; gene;
KW human.
XX
OS Homo sapiens.
XX
PN US2003181649-A1.
XX
PD 25-SEP-2003.
XX
PF 07-MAY-2002; 2002US-00063640.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.

```
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-875162/81.
DR   P-PSDB; ADH38051.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Example 4; SEQ ID NO 135; 397pp; English.
XX
CC   This invention describes novel human PRO polypeptides and the
CC   polynucleotides encoding them which have cytostatic, antidiabetic,
CC   antiarthritic, osteopathic and antirheumatic activity. Specifically
CC   claimed are secreted and transmembrane polypeptides, e.g. PRO180, PRO218,
CC   PRO263, PRO295, PRO874, PRO300, PRO1864, PRO1282, PRO1063 or PRO1773
CC   polypeptide. The PRO polypeptides or anti-PRO antibodies are useful for
CC   preparing a medicament for treating a condition that is responsive to the
CC   PRO polypeptide or anti-PRO antibody e.g. cancer, diabetes,
CC   osteoarthritis or rheumatoid arthritis. PRO nucleotide sequences may be
CC   used as hybridisation probes in chromosome and gene mapping or in
CC   generating antisense RNA and DNA. The PRO nucleic acids are also useful
CC   in preparing PRO polypeptides, in assays to identify other proteins or
CC   molecules involved in binding reaction, in generating transgenic animals
CC   or knockout animals, which in turn are useful in the development and
CC   screening of therapeutically useful reagents, for chromosome
CC   identification and tissue typing. The PRO polypeptides and nucleic acid
CC   molecules are also useful in gene therapy, and as molecular weight
CC   markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC   used in diagnostic assays for PRO, or for the affinity purification of
CC   PRO from recombinant cell culture or natural sources. This sequence
CC   encodes a PRO polypeptide described in the disclosure of the invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:          884
Score:                    1242.00         Matches:         242
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       10              Gaps:            0

US-10-063-743-136 (1-242) x ADH38050 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 32
ADH57470
ID   ADH57470 standard; cDNA; 884 BP.
XX
AC   ADH57470;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   human; PRO; membrane bound protein; membrane bound receptor;
KW   cell proliferation; cell migration; cell differentiation;
KW   mitogenic factor; survival factor; cytotoxic factor;
KW   differentiation factor; neuropeptide; hormone; cell receptor;
KW   receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS   Homo sapiens.
XX
```

PN US2003180920-A1.
XX
PD 25-SEP-2003.
XX
PF 08-MAY-2002; 2002US-00063728.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-830995/77.
DR P-PSDB; ADH57471.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; Fig 135; 397pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH57470 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 33
ADH53612
ID ADH53612 standard; cDNA; 884 BP.

XX
AC ADH53612;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003181636-A1.
XX
PD 25-SEP-2003.
XX
PF 02-MAY-2002; 2002US-00063523.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-875157/81.
DR P-PSDB; ADH53613.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH53612 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623
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Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
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Db        744 AGGAGG 749
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RESULT 34
ADH53782
ID ADH53782 standard; cDNA; 884 BP.
XX
AC ADH53782;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003181641-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063589.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-875161/81.
DR P-PSDB; ADH53783.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH53782 (1-884)

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Qy-         1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
                  ||||||
Db        744 AGGAGG 749
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RESULT 35
ADH52118
ID ADH52118 standard; cDNA; 884 BP.
XX
AC ADH52118;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003181638-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063579.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-875158/81.
DR P-PSDB; ADH52119.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH52118 (1-884)

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Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 36
ADH49973
ID ADH49973 standard; cDNA; 884 BP.
XX
AC ADH49973;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003181639-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063581.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-875159/81.
DR P-PSDB; ADH49974.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; Fig 135; 397pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
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CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
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CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

```
Query Match:          100.00%       Indels:        0
DB:                   10            Gaps:          0

US-10-063-743-136 (1-242) x ADH49973 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
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Db        744 AGGAGG 749

RESULT 37
ADI25483
ID   ADI25483 standard; cDNA; 884 BP.
XX
AC   ADI25483;
XX
DT   15-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003181696-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063536.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-875175/81.
DR   P-PSDB; ADI25484.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC   The invention relates to a novel PRO (secreted and transmembrane protein)
CC   polypeptide, and the polynucleotide sequence encoding it. Also included
CC   are a vector comprising the novel nucleic acid and a host cell comprising
CC   the vector. The polynucleotide sequence is useful in molecular biology as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA, and in gene therapy. The polynucleotide sequence
CC   may also be used in preparing the PRO polypeptide by recombinant
CC   techniques, and in generating either transgenic or knock-out animals
CC   which, in turn, are useful in the development and screening of
CC   therapeutically useful reagents. The PRO polynucleotide sequence is
CC   useful in preparing a medicament for treating a condition responsive to
CC   the polypeptide or antibody, such as tumours, and in various diagnostic
CC   assays. The specification also discloses other PRO proteins and the
CC   polynucleotide sequences encoding them. The present sequence encodes a
CC   PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              6.1e-126        Length:         884
Score:                  1242.00         Matches:        242
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-063-743-136 (1-242) x ADI25483 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 38
ADH90276
ID   ADH90276 standard; cDNA; 884 BP.
XX
AC   ADH90276;
XX
DT   15-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003181698-A1.
XX
PD   25-SEP-2003.
XX
PF   07-MAY-2002; 2002US-00063638.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-875177/81.
DR   P-PSDB; ADH90277.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC   The invention relates to a novel PRO (secreted and transmembrane protein)
CC   polypeptide, and the polynucleotide sequence encoding it. Also included
CC   are a vector comprising the novel nucleic acid and a host cell comprising
CC   the vector. The polynucleotide sequence is useful in molecular biology as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA, and in gene therapy. The polynucleotide sequence
CC   may also be used in preparing the PRO polypeptide by recombinant
CC   techniques, and in generating either transgenic or knock-out animals
CC   which, in turn, are useful in the development and screening of
CC   therapeutically useful reagents. The PRO polynucleotide sequence is
CC   useful in preparing a medicament for treating a condition responsive to
```

```
CC   the polypeptide or antibody, such as tumours, and in various diagnostic
CC   assays. The specification also discloses other PRO proteins and the
CC   polynucleotide sequences encoding them. The present sequence encodes a
CC   PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:         884
Score:                    1242.00         Matches:        242
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       10              Gaps:           0

US-10-063-743-136 (1-242) x ADH90276 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 39
ADI25653
ID   ADI25653 standard; cDNA; 884 BP.
XX
AC   ADI25653;
XX
DT   15-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003181669-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063570.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-811661/76.
DR   P-PSDB; ADI25654.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC   The invention describes an antibody that specifically binds to a PRO
CC   polypeptide having a fully defined amino acid sequence given in the
CC   specification. The antibody is useful in identifying PRO polypeptides
CC   useful for various industrial applications, including pharmaceuticals,
```

CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADI25653 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 40

ADH97827
ID ADH97827 standard; cDNA; 884 BP.
XX
AC ADH97827;
XX
DT 15-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003181672-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063592.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-852263/79.
DR P-PSDB; ADH97828.
XX
PT Novel antibody that binds to a PRO polypeptide, useful for treating
PT cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT specific cells, tissues, or serum.
XX
PS Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC The invention relates to a PRO (secreted and transmembrane protein)

```
CC   polynucleotide appearing as ADH97773 encoding PRO polypeptide having
CC   appearing as ADH97773. Also included are a vector comprising the novel
CC   nucleic acid and a host cell comprising the vector. The polynucleotide is
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC   gene therapy. The polynucleotide may also be used in preparing PRO
CC   polypeptides by recombinant techniques, and in generating either
CC   transgenic animals or knock-out animals which, in turn, are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polynucleotide is used in preparing a medicament for treating a condition
CC   responsive to the polypeptide or antibody, such as tumours, and in
CC   various diagnostic assays. The specification discloses 84 PRO proteins
CC   and 84 PRO polynucleotides. The present sequence encodes a PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:         884
Score:                    1242.00         Matches:        242
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       10              Gaps:           0

US-10-063-743-136 (1-242) x ADH97827 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 41
ADI03675
ID   ADI03675 standard; cDNA; 884 BP.
XX
AC   ADI03675;
XX
DT   22-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   PRO; human; secreted; transmembrane; antiarthritic; antidiabetic;
KW   cytostatic; vulnerary; hyperglycaemic; hypoglycaemic; bone disorder;
KW   cartilage disorder; sports injury; arthritis; glucose uptake; diabetes;
KW   pericyte-associated tumour; wound healing; cancer; gene therapy; ss;
KW   gene.
XX
OS   Homo sapiens.
XX
PN   US2003181656-A1.
XX
PD   25-SEP-2003.
XX
PF   07-MAY-2002; 2002US-00063659.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-875169/81.
```

```
DR   P-PSDB; ADI03676.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Example 4; Fig 135; 397pp; English.
XX
CC   This invention describes a novel human secreted and transmembrane PRO
CC   polypeptide and the polynucleotides encoding it which have antiarthritic,
CC   antidiabetic, cytostatic, vulnerary, hyperglycaemic and hypoglycaemic
CC   activity. The PRO polypeptides are useful for treating various bone
CC   and/or cartilage disorders, for example, sports injuries and arthritis.
CC   They are also useful in the therapeutic treatment of disorders where
CC   either the stimulation or inhibition of glucose uptake by skeletal muscle
CC   would be beneficial, for example, diabetes or hyper- or hypo-
CC   insulineamia. They are also useful for treating pericyte-associated
CC   tumours and in wound healing. An anti-PRO antibody is useful for the
CC   preparation of a medicament useful in the treatment of cancer. The PRO
CC   polypeptides are also useful as molecular weight markers, or for
CC   chromosome identification. The PRO genes are useful as hybridisation
CC   probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC   The PRO genes may also be used in gene therapy, particularly for
CC   replacing a defective gene. ADI03541-ADI03708 represent the PRO
CC   polynucleotides and polypeptides described in the disclosure of the
CC   invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126      Length:          884
Score:                    1242.00       Matches:         242
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0

US-10-063-743-136 (1-242) x ADI03675 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 42
ADI12032
ID   ADI12032 standard; cDNA; 884 BP.
XX
AC   ADI12032;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human PRO polynucleotide #68.
XX
KW   Human; PRO; gene; ss; cancer; affinity purification; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003181686-A1.
XX
PD   25-SEP-2003.
XX
PF   03-MAY-2002; 2002US-00063584.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-852271/79.
DR   P-PSDB; ADI12033.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 395pp; English.
XX
CC   The invention relates to an antibody that binds to a human PRO
CC   polypeptide. The invention also relates to human PRO polynucleotides
CC   encoding the PRO polypeptides of the invention. The antibody is
CC   preferably a monoclonal or humanised antibody, or an antibody fragment,
CC   and is used to treat cancer. The anti-PRO antibody can be used in
CC   diagnostic assays, e.g. for detecting PRO expression in specific cells,
CC   tissues or serum. The anti-PRO antibodies are also useful for the
CC   affinity purification of PRO from recombinant cell culture or natural
CC   sources. This sequence represents a human PRO polynucleotide of the
CC   invention.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126      Length:          884
Score:                    1242.00       Matches:         242
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       10            Gaps:            0
```

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US-10-063-743-136 (1-242) x ADI12032 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 43
ADH90106
ID   ADH90106 standard; cDNA; 884 BP.
XX
AC   ADH90106;
XX
DT   22-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003181697-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063562.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380139.
PR   25-AUG-1999;   99US-00380142.
PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-875176/81.
DR   P-PSDB; ADH90107.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC   The invention relates to a novel PRO (secreted and transmembrane protein)
CC   polypeptide, and the polynucleotide sequence encoding it. Also included
CC   are a vector comprising the novel nucleic acid and a host cell comprising
CC   the vector. The polynucleotide sequence is useful in molecular biology as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA, and in gene therapy. The polynucleotide sequence
CC   may also be used in preparing the PRO polypeptide by recombinant
CC   techniques, and in generating either transgenic or knock-out animals
CC   which, in turn, are useful in the development and screening of
CC   therapeutically useful reagents. The PRO polynucleotide sequence is
CC   useful in preparing a medicament for treating a condition responsive to
CC   the polypeptide or antibody, such as tumours, and in various diagnostic
CC   assays. The specification also discloses other PRO proteins and the
CC   polynucleotide sequences encoding them. The present sequence encodes a
CC   PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
```

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH90106 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 44
ADH98507
ID ADH98507 standard; cDNA; 884 BP.
XX
AC ADH98507;
XX
DT 22-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003181707-A1.
XX
PD 25-SEP-2003.
XX
PF 01-MAY-2002; 2002US-00063514.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-802902/75.
DR P-PSDB; ADH98508.
XX
PT New isolated PRO polypeptide, useful for treating various bone and/or
PT cartilage disorders, for example, sports injuries and arthritis.
XX
PS Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC The invention relates to a PRO (secreted and transmembrane protein)
CC polynucleotide appearing as ADH98453 encoding PRO polypeptide having
CC appearing as ADH98453. Also included are a vector comprising the novel
CC nucleic acid and a host cell comprising the vector. The polynucleotide is
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polynucleotide is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The specification discloses 84 PRO proteins
CC and 84 PRO polynucleotides. The present sequence encodes a PRO protein.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH98507 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 45
ADI11182
ID ADI11182 standard; cDNA; 884 BP.
XX
AC ADI11182;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PRO polynucleotide #68.
XX
KW Human; PRO; gene; ss; cancer; affinity purification; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003181682-A1.
XX
PD 25-SEP-2003.
XX
PF 07-MAY-2002; 2002US-00063651.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-875174/81.
DR P-PSDB; ADI11183.
XX
PT Novel antibody that binds to a PRO polypeptide, useful for treating
PT cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT specific cells, tissues, or serum.
XX
PS Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC The invention relates to an antibody that binds to a human PRO
CC polypeptide. The invention also relates to human PRO polynucleotides
CC encoding the PRO polypeptides of the invention. The antibody is
CC preferably a monoclonal or humanised antibody, or an antibody fragment,
CC and is used to treat cancer. The anti-PRO antibody can be used in
CC diagnostic assays, e.g. for detecting PRO expression in specific cells,
CC tissues or serum. The anti-PRO antibodies are also useful for the
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. This sequence represents a human PRO polynucleotide of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADI11182 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
                ||||||
Db        744 AGGAGG 749
```

RESULT 46
ADI11692
ID ADI11692 standard; cDNA; 884 BP.
XX
AC ADI11692;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PRO polynucleotide #68.
XX
KW Human; PRO; gene; ss; cancer; affinity purification; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003181684-A1.
XX
PD 25-SEP-2003.
XX
PF 07-MAY-2002; 2002US-00063660.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-852269/79.
DR P-PSDB; ADI11693.
XX
PT Novel antibody that binds to a PRO polypeptide, useful for treating
PT cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT specific cells, tissues, or serum.
XX
PS Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC The invention relates to an antibody that binds to a human PRO
CC polypeptide. The invention also relates to human PRO polynucleotides
CC encoding the PRO polypeptides of the invention. The antibody is
CC preferably a monoclonal or humanised antibody, or an antibody fragment,
CC and is used to treat cancer. The anti-PRO antibody can be used in
CC diagnostic assays, e.g. for detecting PRO expression in specific cells,
CC tissues or serum. The anti-PRO antibodies are also useful for the
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. This sequence represents a human PRO polynucleotide of the
CC invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADI11692 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323
```

```
Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 47
ADH98337
ID   ADH98337 standard; cDNA; 884 BP.
XX
AC   ADH98337;
XX
DT   22-APR-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   affinity purification; secreted and transmembrane protein.
XX
OS   Homo sapiens.
XX
PN   US2003181709-A1.
XX
PD   25-SEP-2003.
XX
PF   02-MAY-2002; 2002US-00063529.
XX
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR   WPI; 2003-802903/75.
DR   P-PSDB; ADH98338.
XX
PT   New isolated PRO polypeptide, useful for treating various bone and/or
PT   cartilage disorders, for example, sports injuries and arthritis.
XX
PS   Disclosure; SEQ ID NO 135; 397pp; English.
XX
CC   The invention relates to a PRO (secreted and transmembrane protein)
CC   polynucleotide appearing as ADH98283 encoding PRO polypeptide having
CC   appearing as ADH98283. Also included are a vector comprising the novel
CC   nucleic acid and a host cell comprising the vector. The polynucleotide is
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC   gene therapy. The polynucleotide may also be used in preparing PRO
CC   polypeptides by recombinant techniques, and in generating either
CC   transgenic animals or knock-out animals which, in turn, are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polynucleotide is used in preparing a medicament for treating a condition
CC   responsive to the polypeptide or antibody, such as tumours, and in
CC   various diagnostic assays. The specification discloses 84 PRO proteins
CC   and 84 PRO polynucleotides. The present sequence encodes a PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.1e-126        Length:          884
Score:                    1242.00         Matches:         242
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       10              Gaps:            0

US-10-063-743-136 (1-242) x ADH98337 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 48
ADH98677
ID ADH98677 standard; cDNA; 884 BP.
XX
AC ADH98677;
XX
DT 22-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003181708-A1.
XX
PD 25-SEP-2003.
XX
PF 01-MAY-2002; 2002US-00063516.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-787568/74.
DR P-PSDB; ADH98678.
XX
PT Novel antibody that binds to a PRO polypeptide, useful for treating
PT cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT specific cells, tissues, or serum.
XX
PS Disclosure; SEQ ID NO 135; 395pp; English.
XX
CC The invention relates to a PRO (secreted and transmembrane protein)
CC polynucleotide appearing as ADH98623 encoding PRO polypeptide having
CC appearing as ADH98623. Also included are a vector comprising the novel
CC nucleic acid and a host cell comprising the vector. The polynucleotide is
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polynucleotide is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The specification discloses 84 PRO proteins
CC and 84 PRO polynucleotides. The present sequence encodes a PRO protein.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADH98677 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
```

RESULT 49
ADH98167
ID ADH98167 standard; cDNA; 884 BP.
XX
AC ADH98167;
XX
DT 22-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW ss; gene; human; PRO; pharmaceutical; diagnostic; biosensor; bioreactor;
KW affinity purification; secreted and transmembrane protein.
XX
OS Homo sapiens.
XX
PN US2003181673-A1.
XX
PD 25-SEP-2003.
XX
PF 03-MAY-2002; 2002US-00063597.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.

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PR   15-SEP-1999;   99US-00397342.
PR   18-OCT-1999;   99US-00403297.
PR   12-NOV-1999;   99US-00423844.
PR   30-DEC-1999;   99WO-US031274.
PR   18-FEB-2000; 2000WO-US004341.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   21-MAR-2000; 2000WO-US007532.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   30-MAY-2001; 2001US-00870574.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   29-JUN-2001; 2001US-00869599.
PR   18-JUL-2001; 2001US-00908827.
PR   06-DEC-2001; 2001US-00006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-852264/79.
DR   P-PSDB; ADH98168.
XX
PT   Novel antibody that binds to a PRO polypeptide, useful for treating
PT   cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT   specific cells, tissues, or serum.
XX
PS   Disclosure; SEQ ID NO 135; 396pp; English.
XX
CC   The invention relates to a PRO (secreted and transmembrane protein)
CC   polynucleotide appearing as ADH98113 encoding PRO polypeptide having
CC   appearing as ADH98113. Also included are a vector comprising the novel
CC   nucleic acid and a host cell comprising the vector. The polynucleotide is
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC   gene therapy. The polynucleotide may also be used in preparing PRO
CC   polypeptides by recombinant techniques, and in generating either
CC   transgenic animals or knock-out animals which, in turn, are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polynucleotide is used in preparing a medicament for treating a condition
CC   responsive to the polypeptide or antibody, such as tumours, and in
CC   various diagnostic assays. The specification discloses 84 PRO proteins
CC   and 84 PRO polynucleotides. The present sequence encodes a PRO protein.
XX
SQ   Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.1e-126        Length:         884
Score:                  1242.00         Matches:        242
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-10-063-743-136 (1-242) x ADH98167 (1-884)

Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749

RESULT 50
ADI05155
ID   ADI05155 standard; cDNA; 884 BP.
XX
AC   ADI05155;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1926 cDNA.
XX
KW   antibody; human; secreted; transmembrane; PRO; cytostatic; cancer; ss;
KW   gene.
XX
OS   Homo sapiens.
XX
PN   US2003180848-A1.
XX
PD   25-SEP-2003.
XX
PF   08-MAY-2002; 2002US-00063694.
XX
PR   30-DEC-1998;   98KR-00062142.
PR   08-MAR-1999;   99WO-US005028.
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PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-802876/75.
DR P-PSDB; ADI05156.
XX
PT Novel antibody that binds to a PRO polypeptide, useful for treating
PT cancer and in diagnostic assays, for e.g. detecting PRO expression in
PT specific cells, tissues, or serum.
XX
PS Example 4; SEQ ID NO 135; 397pp; English.
XX
CC This invention describes a novel antibody that binds to a human secreted
CC and transmembrane PRO polypeptide which is a monoclonal antibody, a
CC humanised antibody, or antibody fragment and is preferably labelled. The
CC antibody has cytostatic activity and can be used to treat cancer. The
CC anti-PRO antibody can be used in diagnostic assays, for e.g. detecting
CC PRO expression in specific cells, tissues, or serum. The anti-PRO
CC antibodies are also useful for the affinity purification of PRO from
CC recombinant cell culture or natural sources. ADI05021-ADI05188 represent
CC human PRO polynucleotides and polypeptides described in the disclosure of
CC the invention.
XX
SQ Sequence 884 BP; 219 A; 185 C; 248 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.1e-126	Length:	884
Score:	1242.00	Matches:	242
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-063-743-136 (1-242) x ADI05155 (1-884)

```
Qy          1 MetAlaAlaAlaLeuTrpGlyPhePheProValLeuLeuLeuLeuLeuSerGlyAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTGCTGCTGCTATCGGGGGAT 83

Qy         21 ValGlnSerSerGluValProGlyAlaAlaAlaGluGlySerGlyGlySerGlyValGly 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGGGAGTGGGGTCGGC 143

Qy         41 IleGlyAspArgPheLysIleGluGlyArgAlaValValProGlyValLysProGlnAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGCCTCAGGAC 203

Qy         61 TrpIleSerAlaAlaArgValLeuValAspGlyGluGluHisValGlyPheLeuLysThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAGACA 263

Qy         81 AspGlySerPheValValHisAspIleProSerGlySerTyrValValGluValValSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCT 323

Qy        101 ProAlaTyrArgPheAspProValArgValAspIleThrSerLysGlyLysMetArgAla 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCA 383

Qy        121 ArgTyrValAsnTyrIleLysThrSerGluValValArgLeuProTyrProLeuGlnMet 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 AGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATG 443

Qy        141 LysSerSerGlyProProSerTyrPheIleLysArgGluSerTrpGlyTrpThrAspPhe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTT 503

Qy        161 LeuMetAsnProMetValMetMetMetValLeuProLeuLeuIlePheValLeuLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CTAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCT 563

Qy        181 LysValValAsnThrSerAspProAspMetArgArgGluMetGluGlnSerMetAsnMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAAGTGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATG 623

Qy        201 LeuAsnSerAsnHisGluLeuProAspValSerGluPheMetThrArgLeuPheSerSer 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTGAATTCCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCA 683

Qy        221 LysSerSerGlyLysSerSerSerGlySerSerLysThrGlyLysSerGlyAlaGlyLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AAATCATCTGGCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAA 743

Qy        241 ArgArg 242
              ||||||
Db        744 AGGAGG 749
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Search completed: December 24, 2004, 20:44:00
Job time : 512 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 24, 2004, 19:01:03 ; Search time 409 Seconds
(without alignments)
340.442 Million cell updates/sec

Title: US-10-063-743-136
Perfect score: 1242
Sequence: 1 MAAALWGFFPVLLLLLLSGD.....SGKSSSGSSKTGKSGAGKRR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1242	100.0	242	2	Q9NPA0	Q9npa0 homo sapien
2	1242	100.0	242	2	AAQ88810	Aaq88810 homo sapi
3	1198	96.5	234	2	Q96ED5	Q96ed5 homo sapien
4	1195.5	96.3	241	2	Q9EP72	Q9ep72 mus musculu
5	456	36.7	262	2	Q7Q7Q1	Q7q7q1 anopheles g
6	412	33.2	222	1	YLC1_CAEEL	Q8wqg1 caenorhabdi
7	372	30.0	75	2	Q91VV9	Q91vv9 mus musculu
8	365	29.4	245	2	Q9V7I0	Q9v7i0 drosophila
9	202.5	16.3	202	2	Q8VY97	Q8vy97 arabidopsis
10	199.5	16.1	210	2	Q84JM6	Q84jm6 arabidopsis
11	194.5	15.7	198	2	Q9SIR2	Q9sir2 arabidopsis
12	164.5	13.2	273	2	Q9P3D1	Q9p3d1 neurospora
13	118	9.5	219	2	Q6CA62	Q6ca62 yarrowia li
14	102.5	8.3	189	2	O94694	O94694 schizosacch
15	98.5	7.9	752	2	Q6LKL3	Q6lkl3 photobacter
16	98.5	7.9	752	2	CAG22133	Cag22133 photobact
17	97.5	7.9	205	2	Q8IEL0	Q8iel0 plasmodium
18	95.5	7.7	411	2	Q9SGX7	Q9sgx7 arabidopsis
19	94.5	7.6	250	2	Q8N9Q3	Q8n9q3 homo sapien
20	94.5	7.6	614	2	Q9F3S1	Q9f3s1 wautersia m
21	94	7.6	259	2	Q931A2	Q931a2 rhizobium m
22	94	7.6	487	2	Q6L2Q5	Q612q5 picrophilus
23	93.5	7.5	526	2	Q7K7B1	Q7k7b1 drosophila
24	93.5	7.5	608	2	O96825	O96825 drosophila
25	93.5	7.5	608	2	Q8MT40	Q8mt40 drosophila
26	93.5	7.5	608	2	AAF57936	Aaf57936 drosophil
27	93	7.5	649	2	Q6BZ08	Q6bz08 debaryomyce
28	93	7.5	3112	2	Q9NKP1	Q9nkp1 leishmania
29	92	7.4	877	2	Q87FT5	Q87ft5 vibrio para
30	91.5	7.4	372	2	Q7KA42	Q7ka42 drosophila
31	91.5	7.4	372	2	Q9U1I8	Q9u1i8 drosophila
32	91.5	7.4	372	2	AAF57408	Aaf57408 drosophil
33	91.5	7.4	702	2	Q7Q9V5	Q7q9v5 anopheles g
34	91.5	7.4	896	2	Q55544	Q55544 synechocyst
35	90.5	7.3	642	2	Q898I0	Q898i0 clostridium
36	90	7.2	283	2	Q73XG0	Q73xg0 mycobacteri
37	90	7.2	283	2	AAS04666	Aas04666 mycobacte
38	90	7.2	481	2	Q9HJA8	Q9hja8 thermoplasm
39	89.5	7.2	768	2	Q7Q394	Q7q394 anopheles g
40	89.5	7.2	1087	1	DP2L_THEAC	Q9hm33 thermoplasm
41	88	7.1	659	2	Q8W131	Q8w131 skeletonema
42	87.5	7.0	383	2	Q8TU49	Q8tu49 methanosarc
43	87.5	7.0	889	2	Q9AAZ6	Q9aaz6 caulobacter
44	87	7.0	273	2	Q97AZ2	Q97az2 thermoplasm
45	86.5	7.0	303	2	Q6CTM4	Q6ctm4 kluyveromyc

ALIGNMENTS

RESULT 1
Q9NPA0
ID Q9NPA0 PRELIMINARY; PRT; 242 AA.
AC Q9NPA0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ATG/GTP binding protein precursor (Hypothetical protein ORF3)
DE (AAAL905) (HT022).
GN Name=ORF3; ORFNames=UNQ905;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Ievolella C., Lanfranchi G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334234; PubMed=10873569;
RA O'Brien K.P., Tapia-Paez I., Stahle-Backdahl M., Kedra D.,
RA Dumanski J.P.;
RT "Five novel human genes in the 11q13-q22 region.";
RL Biochem. Biophys. Res. Commun. 273:90-94(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Xu X., Yang Y., Gao G., Xiao H., Chen Z., Han Z.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ245874; CAC01611.1; -.
DR EMBL; AJ250344; CAB96539.1; -.
DR EMBL; AY358445; AAQ88810.1; -.
DR EMBL; AF242729; AAG44477.1; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0017076; F:purine nucleotide binding; NAS.
DR InterPro; IPR008969; CarboxypepD_reg.

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KW   Hypothetical protein; Signal.
FT   SIGNAL       1     20       Potential.
FT   CHAIN       21    242       putative ATG/GTP binding protein.
SQ   SEQUENCE   242 AA;  26470 MW;  A71930B89A4C2458 CRC64;

  Query Match             100.0%;  Score 1242;  DB 2;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-98;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 2
AAQ88810
ID   AAQ88810    PRELIMINARY;      PRT;   242 AA.
AC   AAQ88810;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   AAAL905.
GN   UNQ905.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT   Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT   Bioinformatics Assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358445; AAQ88810.1; -.
SQ   SEQUENCE   242 AA;  26470 MW;  A71930B89A4C2458 CRC64;

  Query Match             100.0%;  Score 1242;  DB 2;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-98;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240

Qy        241 RR 242
              ||
Db        241 RR 242


RESULT 3
Q96ED5
ID   Q96ED5      PRELIMINARY;      PRT;   234 AA.
AC   Q96ED5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C15orf24 protein (Fragment).
GN   Name=C15orf24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012456; AAH12456.1; -.
DR   InterPro; IPR008969; CarboxypepD_reg.
FT   NON_TER      1      1
SQ   SEQUENCE   234 AA;  25622 MW;  2561AD5DA2EA1FFF CRC64;

  Query Match             96.5%;  Score 1198;  DB 2;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-94;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 FPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAARVL 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAARVL 60

Qy         69 VDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKT 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKT 120
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Qy        129 SEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDP 180

Qy        189 DMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR 234


RESULT 4
Q9EP72
ID   Q9EP72      PRELIMINARY;      PRT;   241 AA.
AC   Q9EP72;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein ORF3 (Mus musculus 2 days neonate thymus thymic
DE   cells cDNA, RIKEN full-length enriched library, clone:E430024O15
DE   product:PUTATIVE ATG/GTP BINDING PROTEIN (HT022) homolog).
GN   Name=2900064A13Rik; Synonyms=ORF3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   O'Brien K.P., Tapia-Paez I., Kedra D., Dumanski J.P.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Ievolella C., Campagna D., Lanfranchi G.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ250345; CAC16213.1; -.
DR   EMBL; AJ278128; CAC01616.1; -.
DR   EMBL; AK088738; BAC40540.1; -.
DR   MGD; MGI:1920274; 2900064A13Rik.
DR   InterPro; IPR008969; CarboxypepD_reg.
KW   Hypothetical protein.
SQ   SEQUENCE   241 AA;  26310 MW;  B1973DD3B3F91764 CRC64;

  Query Match             96.3%;  Score 1195.5;  DB 2;  Length 241;
  Best Local Similarity   96.3%;  Pred. No. 3.5e-94;
  Matches  233;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQD 60
              || |||||| | ||||||||  |||||||||| ||||||:||||||||||||||||||||
Db          1 MAGALWGFFSV-LLLLLSGDAHSSEVPGAAAEGPGGSGVGLGDRFKIEGRAVVPGVKPQD 59

Qy         61 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRA 120
              ||||||||||||||||||||||||||||||||||||||||:||||:||||||||||||||
Db         60 WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVISPAYKFDPVRVDITSKGKMRA 119

Qy        121 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 RYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLP 179

Qy        181 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 KVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGK 239

Qy        241 RR 242
              ||
Db        240 RR 241


RESULT 5
Q7Q7Q1
ID   Q7Q7Q1      PRELIMINARY;      PRT;   262 AA.
AC   Q7Q7Q1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP4451 (Fragment).
GN   Name=agCG56943; ORFNames=ENSANGG00000019103;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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CC       preliminary data.
DR   EMBL; AAAB01008952; EAA10592.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   262 AA;  29846 MW;  910AA9B781068CC0 CRC64;

  Query Match             36.7%;  Score 456;  DB 2;  Length 262;
  Best Local Similarity   45.4%;  Pred. No. 9e-31;
  Matches   89;  Conservative   48;  Mismatches   49;  Indels   10;  Gaps    4;

Qy         44 RFKIEGRAVVPGVKPQD----WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVV 99
              |: ||||   | :   |    |    :: ::| |: |||: ||||::  :|||||||:|
Db         59 RYAIEGRVYPPELYGGDPDLAWQLDTQISINGGEYKGFLREDGSFLISSVPSGSYVVEIV 118

Qy        100 SPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTD 159
              :| | ::||||:|  ||| ||| :||:: |:|::|||||::|:     || :|| |  ||
Db        119 NPDYFYEPVRVEINPKGKFRARKLNYVQPSQVLQLPYPLKLKALTRFRYFQQREQWKITD 178

Qy        160 FLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFS 219
              || ||||:||:||| | ::|||::  |||: ::||| ::|:    ::||: || :|  |
Db        179 FLFNPMVLMMILPLGIMLILPKIM--SDPETKKEME-NLNLSKMTNDLPEFSEMLTSYF- 234

Qy        220 SKSSGKSSSGSSKTGK 235
                :|| ::: ::| ||
Db        235 --TSGSAAAAAAKAGK 248


RESULT 6
YLC1_CAEEL
ID   YLC1_CAEEL     STANDARD;      PRT;   222 AA.
AC   Q8WQG1; Q18491;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Hypothetical protein C35D10.1 in chromosome III.
GN   ORFNames=C35D10.1;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Fulton L.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   REVISIONS.
RA   Waterston R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO DROSOPHILA CG8397.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U21324; AAK93840.2; -.
DR   WormPep; C35D10.1; CE29951.
KW   Hypothetical protein.
SQ   SEQUENCE   222 AA;  24963 MW;  951F3132BD88F15C CRC64;

  Query Match             33.2%;  Score 412;  DB 1;  Length 222;
  Best Local Similarity   39.7%;  Pred. No. 4.4e-27;
  Matches   79;  Conservative   50;  Mismatches   62;  Indels    8;  Gaps    4;

Qy         45 FKIEGRAVVPGVKP-QDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAY 103
              | :||   :|  :    | : ||: ::  :::||:: | :| |  :|:|:|:|:: :  :
Db         30 FSVEGEIALPSTRNCAKWSAGARIHLNHGQYMGFVRQDCTFRVDFVPTGTYIVQIENTDF 89

Qy        104 RFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMN 163
               |:|:|||||||||||||| :  :: : |  |||||:: : ||  || ||| |  || | :

Db         90 VFEPIRVDITSKGKMRARKLTILQPNNVNTLPYPLRLSARGPARYFRKREEWRITDMLFS 149

Qy        164 PMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSS 223
              |||:|:|:||:: ::||| :  :||:::|||   ||     ::||| | |   |   :
Db        150 PMVLMLVVPLVVMLILPK-MTANDPELKKEME---NMQMPKVDMPDVGEMMANFFGGSAP 205

Qy        224 GKSSSGSSKTGKSGAGKRR 242
                |     : || ||:|:||
Db        206 AKK---KAVTGGSGSGQRR 221


RESULT 7
Q91VV9
ID   Q91VV9      PRELIMINARY;      PRT;   75 AA.
AC   Q91VV9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   2900064A13Rik protein.
GN   Name=2900064A13Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008164; AAH08164.1; -.
DR   MGD; MGI:1920274; 2900064A13Rik.
SQ   SEQUENCE   75 AA;  8293 MW;  6D899EA38D247FE3 CRC64;

  Query Match             30.0%;  Score 372;  DB 2;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-24;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        168 MMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSS 227
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSS 60

Qy        228 SGSSKTGKSGAGKRR 242
              |||||||||||||||
Db         61 SGSSKTGKSGAGKRR 75


RESULT 8
Q9V7I0
ID   Q9V7I0      PRELIMINARY;      PRT;   245 AA.
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AC   Q9V7I0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   CG8397-PA.
GN   ORFNames=CG8397;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003808; AAF58075.1; -.
DR   FlyBase; FBgn0034066; CG8397.
SQ   SEQUENCE   245 AA;  27794 MW;  10ECF60C87EB22B7 CRC64;

  Query Match             29.4%;  Score 365;  DB 2;  Length 245;
  Best Local Similarity   32.5%;  Pred. No. 5.3e-23;
  Matches   80;  Conservative   53;  Mismatches   65;  Indels   48;  Gaps    6;

Qy          1 MAAALWGFFPVLLL----LLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGV 56
              |  |: |  :| |    :::  |    || |                 : ||||     |
Db          1 MCLKLFVFTALLALVSCEVIIGQDELVDEVSGL--------------YTIEGR-----V 40

Qy         57 KPQD--------------------WISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYV 95
               | |                    | :   : ::  |  ||:: || |::  :|||||:
Db         41 SPPDSIFSPTQGGGRSAPVNKNTPKWHTEITLSINDGEFKGFVREDGQFMISGVPSGSYI 100

Qy         96 VEVVSPAYRFDPVRVDITSKGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESW 155
              ::|  |   ::||||:|  ||| ||| ||::: :::::: |||::|   |  ||  || |
Db        101 LDVHHPDVFYEPVRVEINPKGKFRARKVNFVQPAQIMQVAYPLRVKPLMPFKYFQTREQW 160

Qy        156 GWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSMNMLNSNHELPDVSEFMT 215
              |||| :|||:|||||||: ::|||::|  ||: ::|:: ::      :::|::|| :|
Db        161 KITDFLFSPMVLMMVLPLLLMLVLPKMIN--DPETKKEID-NLQFPKMGNDMPEISEMLT 217

Qy        216 RLFSSK 221
              | : |
Db        218 SLLTGK 223


RESULT 9
Q8VY97
ID   Q8VY97      PRELIMINARY;      PRT;   202 AA.
AC   Q8VY97;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein At4g32130; F10N7.60 (Hypothetical protein
DE   At4g32130).
GN   Name=At4g32130;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA   Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA   Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA   Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA   Ecker J., Theologis A., Davis R.W.;
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RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA   Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA   Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA   Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA   Ecker J., Theologis A., Davis R.W.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY072335; AAL61942.1; -.
DR   EMBL; AY114611; AAM47930.1; -.
DR   InterPro; IPR008969; CarboxypepD_reg.
KW   Hypothetical protein.
SQ   SEQUENCE   202 AA;  22563 MW;  55A8F86DE6FAFDCC CRC64;

  Query Match             16.3%;  Score 202.5;  DB 2;  Length 202;
  Best Local Similarity   28.7%;  Pred. No. 3.5e-09;
  Matches   47;  Conservative   40;  Mismatches   66;  Indels   11;  Gaps    3;

Qy         40 GIGDRFKIEGRAVVPG---VKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVV 96
              |  | : | ||  ||    :      |  :|:::| :|| ||: || |  | :|:|:::: 
Db         29 GSEDSYTITGRVRVPASTVIGHAAKFSNIKVILNGGQHVTFLRPDGYFTFHKVPAGTHLI 88

Qy         97 EVVSPAYRFDPVRVDITS--KGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRES 154
              || :  | | |||||::  :||::|       :|  |    | ::      |:  ||  
Db         89 EVYALGYFFSPVRVDVSARHRGKVQA------TLTETRRSLTELVLEPLRAEQYYEMREP 142

Qy        155 WGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSM 198
             :    : :|| :|:   :::  |:||::   ||:  :  :: |
Db        143 FSVMSIVKSPMGLMVGFMVVVVFLMPKLMENIDPEEMKSAQEQM 186


RESULT 10
Q84JM6
ID   Q84JM6      PRELIMINARY;      PRT;   210 AA.
AC   Q84JM6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein At2g25310.
GN   Name=At2g25310;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT004317; AAO42314.1; -.
DR   EMBL; BT006136; AAP04121.1; -.
DR   InterPro; IPR008969; CarboxypepD_reg.
KW   Hypothetical protein.
SQ   SEQUENCE   210 AA;  23428 MW;  8E6910EB6A1E7A82 CRC64;

  Query Match             16.1%;  Score 199.5;  DB 2;  Length 210;
  Best Local Similarity   27.5%;  Pred. No. 6.7e-09;
  Matches   46;  Conservative   44;  Mismatches   60;  Indels   17;  Gaps    4;

Qy         40 GIGDRFKIEGRAVVPGVKPQDWI------SAARVLVDGEEHVGFLKTDGSFVVHDIPSGS 93
              |  | : | ||  :|   | : |       |  :|:::| : : ||: || |  |::|:|: 
Db         34 GSEDSYTITGRVKIP---PSNVIGHIAKFSNVKVILNGGQKITFLRPDGYFTFHEVPAGT 90

Qy         94 YVVEVVSPAYRFDPVRVDITS--KGKMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIK 151
              :::|| :  | | ||||:::  :||::|       :|  |    | ::      |:  
Db         91 HLIEVSAMGYFFSPVRVDVSARHRGKVQA------TLTETRRSLTELVLEPLKEEQYYEI 144

Qy        152 RESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSM 198
             || :     : :|| :|:   :::  |:||::   ||:  :: :: |
Db        145 REPFNIMSIVKSPMGLMVGFMVVVVFLMPKLMENIDPEEMKQAQEEM 191


RESULT 11
Q9SIR2
ID   Q9SIR2      PRELIMINARY;      PRT;   198 AA.
AC   Q9SIR2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein At2g25310.
GN   Name=At2g25310;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA   Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA   Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA   Fraser C.M., Venter J.C.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Town C.D., Kaul S.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC007070; AAD23660.1; -.
DR   PIR; H84646; H84646.
DR   InterPro; IPR008969; CarboxypepD_reg.
KW   Hypothetical protein.
SQ   SEQUENCE   198 AA;  21907 MW;  88C8AB506FAA0BF8 CRC64;

  Query Match             15.7%;  Score 194.5;  DB 2;  Length 198;
  Best Local Similarity   25.6%;  Pred. No. 1.7e-08;
  Matches   43;  Conservative   46;  Mismatches   48;  Indels   31;  Gaps    5;

Qy         40 GIGDRFKIEGRAVVPGVKPQDWI------SAARVLVDGEEHVGFLKTDGSFVVHDIPSGS 93
              |  | : | ||  :|   | : |       |  :|:::| : : ||: || |  |::|:|: 
Db         34 GSEDSYTITGRVKIP---PSNVIGHIAKFSNVKVILNGGQKITFLRPDGYFTFHEVPAGT 90

Qy         94 YVVEVVSPAYRFDPVRVDITS--KGKMRARYVNYIKT-SEVVRLPYPLQMKSSGPPSYFI 150
              :::|| :  | | ||||:::  :||::|       :: :|::| |: :
Db         91 HLIEVSAMGYFFSPVRVDVSARHRGKVQATLTETRRSLTELIREPFNIM---------- 139

Qy        151 KRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRREMEQSM 198
                       : :|| :|:   :::  |:||::   ||:  :: :: |
Db        140 --------SIVKSPMGLMVGFMVVVVFLMPKLMENIDPEEMKQAQEEM 179


RESULT 12
Q9P3D1
ID   Q9P3D1      PRELIMINARY;      PRT;   273 AA.
AC   Q9P3D1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein B13I18.120.
```

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GN   Name=B13I18.120;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   German Neurospora genome project;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL390189; CAB99182.2; -.
KW   Hypothetical protein.
SQ   SEQUENCE   273 AA;  28815 MW;  A1B150CB0C1A01B1 CRC64;

  Query Match             13.2%;  Score 164.5;  DB 2;  Length 273;
  Best Local Similarity   24.9%;  Pred. No. 9e-06;
  Matches   60;  Conservative   41;  Mismatches   87;  Indels   53;  Gaps   11;

Qy          53 VPGVKPQDWISAARVLVDGEEHVGFLKTDG----------SFVVHDIPSGSYVVEVVSP 101
               :|    | | :|    :    | | | | |          : |  ::  |||::::
Db          34 LPSAPPGD-VSGKLFVFPPSTH-GTLSTFGQTKSAPLSVANTLVFRNVTQGSYLLDIHCA 91

Qy         102 AYRFDPVRVDI--TSKG----------KMRAR-YVNY------IKTSEVVRLPYP---- 137
                : | |:|||:  |  |          |: |: :  |      |  |  |
Db          92 THAFAPLRVDVAPTLDGVLEEGDGHGNVKLEAKAWQTYRGNDWDNKGEEAPRQTLKNGRD 151

Qy         138 ----LQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIFVLLPKVVNTSDPDMRRE 193
                    |  |   ||::|  :     | |||::: :: ::||: :||:|   ||:|| |
Db         152 GGVVFGAKVLGEKGYFMERSKFSILSILRNPMILLGLVSMVIFLGMPKLVENMDPEMRAE 211

Qy         194 MEQS-----MNMLNSNHELP-----DVSEFM--TRLFSSKSSGKSSSGSSKTGKSGAGKR 241
               |::     || |      |     |:: |:  |     :||| ::: :    : |  ||
Db         212 WEENQKKNPMNALMGGGGAPAAPNFDMAAFLAGTSAKKEESSGDAAASTGGGAQQGGKKR 271

Qy         242 R 242
               |
Db         272 R 272


RESULT 13
Q6CA62
ID   Q6CA62      PRELIMINARY;      PRT;   219 AA.
AC   Q6CA62;
DT   01-OCT-2004 (TrEMBLrel. 28, Created)
DT   01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Similar to tr|Q9P3D1 Neurospora crassa Conserved hypothetical
DE   protein.
GN   ORFNames=YALI0D05599g;
OS   Yarrowia lipolytica (Candida lipolytica).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Dipodascaceae; Yarrowia.
OX   NCBI_TaxID=4952;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIB99;
RG   GENOLEVURES;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIB99;
RA   Genoscope;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR382130; CAG80638.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   219 AA;  24199 MW;  8514C9681C1CD0AC CRC64;

  Query Match             9.5%;  Score 118;  DB 2;  Length 219;
  Best Local Similarity   23.0%;  Pred. No. 0.068;
  Matches   42;  Conservative   37;  Mismatches   66;  Indels   38;  Gaps    5;

Qy          56 VKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDP---VRVDI 112
               |:| |  |:|        :  :|: || | : |:  ||| :|: |     |    |:||
Db          43 VEPLDASSSA-------PYKTYLRKDGHFSLQDLSEGSYQLELHSINLALVPPKSYRIDI 95

Qy         113 TSKGKM--RARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMV 170
                :  ::    :  :  :    | ||| :         ::|| :   : | :||::| :
Db          96 VNATELVIHEVFAGHSVSDLGPRASYPLVIGPVARKKLTMEREQFSAFNMLKSPMMLMSL 155

Qy         171 LPLLIFVLLPKVVNTSDPD-----------------MRREMEQSMNMLNSNHELPDVS 211
               |:: | :||:|   ||:                 |:|:: :|         |::
Db         156 GGLIMVVGVPKLVKHLDPEAVAEFQKIQAEKNKKKGPAQSRDMQKQINNF-------DMA 208

Qy         212 EFM 214
               ||:
Db         209 EFL 211


RESULT 14
O94694
ID   O94694      PRELIMINARY;      PRT;   189 AA.
AC   O94694;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   SPBC83.10 protein.
GN   Name=SPBC83.10;
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972h-;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA   Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,
RA   Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA   Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
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RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
DR   EMBL; AL035536; CAB36872.1; -.
DR   PIR; T40699; T40699.
DR   GeneDB_SPombe; SPBC83.10; -.
DR   InterPro; IPR008969; CarboxypepD_reg.
SQ   SEQUENCE   189 AA;  21528 MW;  9A1A1D0D426AE97C CRC64;

  Query Match             8.3%;  Score 102.5;  DB 2;  Length 189;
  Best Local Similarity   19.4%;  Pred. No. 1.2;
  Matches   36;  Conservative   39;  Mismatches   76;  Indels   35;  Gaps    4;

Qy          9 FPVLLLLLLSGDVQSS---EVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWISAA 65
              | :| :|  :| :| |    || |              |:   ::| :    : : |
Db          6 FLLLSVLCFAGCIQQSLQAEVYG----------------KVLTNTILPKINLLSYDTRA 48

Qy         66 RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDI---------TSKG 116
              |::   :     :: ||||   ::|   | : : |  | |    : |         ||
Db         49 RLISSNKTFETVVERDGSFTFPNVPDEIYFLRLESIDYEFSEFHIIINESIVYPYYTSPA 108

Qy        117 KMRARYVNYIKTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMVLPLLIF 176
              : |        :|      ||:::::     |  :   :     | :||::: :  :::
Db        109 EKRP------ASSTAKNTSYPIKVRAVLKRDYLKEPRKFSLIRLLKSPMMLLSLASVVLV 162

Qy        177 VLLPKV 182
               :|||:
Db        163 FILPKL 168


RESULT 15
Q6LKL3
ID   Q6LKL3      PRELIMINARY;      PRT;   752 AA.
AC   Q6LKL3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PBPRB0260;
OS   Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Photobacterium.
OX   NCBI_TaxID=74109;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA   Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA   Valle G.;
RT   "Genome analysis of Photobacterium profundum reveals the complexity of
RT   high pressure adaptations.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR378675; CAG22133.1; -.
DR   InterPro; IPR008979; Gal_bind_like.
DR   InterPro; IPR008928; Glyco_trans_6hp.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   752 AA;  84680 MW;  6FB85B57CDA7D018 CRC64;

  Query Match             7.9%;  Score 98.5;  DB 2;  Length 752;
  Best Local Similarity   23.0%;  Pred. No. 13;
  Matches   47;  Conservative   27;  Mismatches   73;  Indels   57;  Gaps   10;

Qy          5 LWGFF-PVLLLLLLSGDVQSSEVPGAAAEGSGG----------------SGVGIGDRFK 46
              || |:  ||   :   |:|    |   ||| ||                :| ||| :::
Db        423 LWRFYTKVLTDYITLHDLQD---PNGIAEGYGGIFEGSATYNERGEFPIEAGDGIGSQYQ 479

Qy         47 --------IEGRAVVPGVKPQDWISAARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEV 98
                     :| |       : |   |: | |       |   | |   | |  :|| |
Db        480 ATVAYAAMLEARG--DDSDAELWQEKAQKLKD------FFNQDWSIADPDKPLANYVNIV 531

Qy         99 VSPAYR----------FDPVRVDITSKGKMRARYVNYIKTS------EVVRLPYPLQMKS 142
                    |          | |::: ||  |:    |:::|  :           |  ::  :

Db        532 QKDGLRLNDFGKENSWFMPMKL-ITEPGERNNNYLDFISQNLGDGIGTTPEAPNNIEAYT 590

Qy        143 SGPPSYF---IKRESWGWTDFLMN 163
                  | :||       |:| |  ::|:
Db        591 YIPETYFPYNRNEEAWKWMQYIMD 614


Search completed: December 24, 2004, 20:21:10
Job time : 411 secs
```